

PTO/SB/64 (09-04)

Approved for use through 07/31/2006. OMB 0651-0031
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, persons are required to respond to a collection of information unless it displays a valid OMB control number.

**PETITION FOR REVIVAL OF AN APPLICATION FOR PATENT
ABANDONED UNINTENTIONALLY UNDER 37 CFR 1.137(b)**

Docket Number (Optional)

FORS-04447

First named inventor: Michael W. Kaiser

Application No.: 09/684,305

Art Unit: 1637

Filed: 10/06/00

Examiner: Fredman

Title: IMPROVED CLEAVAGE AGENTS

Attention: Office of Petitions

Mail Stop Petition

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

FAX (703) 872-9306

NOTE: If information or assistance is needed in completing this form, please contact Petitions
Information at (703) 305-9282.

The above-identified application became abandoned for failure to file a timely and proper reply to a notice or
action by the United States Patent and Trademark Office. The date of abandonment is the day after the expiration
date of the period set for reply in the office notice or action plus an extensions of time actually obtained.

APPLICANT HEREBY PETITIONS FOR REVIVAL OF THIS APPLICATION

NOTE: A grantable petition requires the following items:

- (1) Petition fee;
- (2) Reply and/or issue fee;
- (3) Terminal disclaimer with disclaimer fee - required for all utility and plant applications
filed before June 8, 1995; and for all design applications; and
- (4) Statement that the entire delay was unintentional.

1. Petition fee☒ Small entity-fee \$ 750.00 (37 CFR 1.17(m)). Applicant claims small entity status. See 37 CFR 1.27.☐ Other than small entity - fee \$ _____ (37 CFR 1.17(m))**2. Reply and/or fee**

A. The reply and/or fee to the above-noted Office action in
the form of Amendment and Subst. Sequence Listing in paper and CRF (identify type of reply):

- ☐ has been filed previously on _____
☒ is enclosed herewith.

B. The issue fee and publication fee (if applicable) of \$ _____.

- ☐ has been paid previously on _____
☐ is enclosed herewith.

[Page 1 of 2]

This collection of information is required by 37 CFR 1.137(b). The information is required to obtain or retain a benefit by the public which is to file (and by the
USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.11 and 1.14. This collection is estimated to take 1.0 hour to
complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any
comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer,
U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED
FORMS TO THIS ADDRESS. SEND TO: Mail Stop Petition, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

01/28/2005 SHINASS1 00000037 09684305

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Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

3. Terminal disclaimer with disclaimer fee

- ☒ Since this utility/plant application was filed on or after June 8, 1995, no terminal disclaimer is required.
- ☐ A terminal disclaimer (and disclaimer fee (37 CFR 1.20(d)) of \$ _____ for a small entity or \$ _____ for other than a small entity) disclaiming the required period of time is enclosed herewith (see PTO/SB/63).

4. STATEMENT: The entire delay in filing the required reply from the due date for the required reply until the filing of a grantable petition under 37 CFR 1.137(b) was unintentional. [NOTE: The United States Patent and Trademark Office may require additional information if there is a question as to whether either the abandonment or the delay in filing a petition under 37 CFR 1.137(b) was unintentional (MPEP 711.03(c), subsections (III)(C) and (D)).]

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Signature

1/24/05

Date

David A. Casimir

Typed or printed name

42,395

Registration Number, if applicable

Medlen & Carroll, 101 Howard Street, Suite 350

Address

608/218-6900

Telephone Number

San Francisco, CA 94105

Address

Enclosures: ☒ Fee Payment

☒ Reply

☐ Terminal Disclaimer Form

☐ Additional sheets containing statements establishing unintentional delay

☐ Other: _____

CERTIFICATE OF MAILING OR TRANSMISSION [37 CFR 1.8(a)]

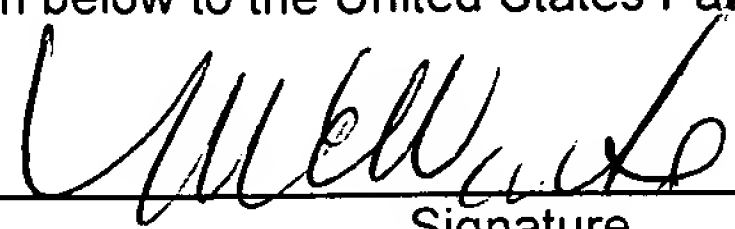
I hereby certify that this correspondence is being:

☒ Deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to: Mail Stop Petition, Commissioner for Patents, P. O. Box 1450, Alexandria, VA 22313-1450.

☐ Transmitted by facsimile on the date shown below to the United States Patent and Trademark Office as (703) 872-9306.

January 24, 2005

Date



Signature

Mary Ellen Waite

Typed or printed name of person signing certificate



PATENT
Attorney Docket No. **FORS-04447**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Michael W. Kaiser *et al.*
Serial No.: 09/684,305
Filed: 10/06/00
Entitled: **Improved Cleavage Agents**

Group No.: 1637
Examiner: Fredman

**TRANSMITTAL FOR REVIVAL OF AN APPLICATION FOR
PATENT ABANDONED UNINTENTIONALLY UNDER 37 C.F.R. 1.137(b)**

Attention: Office of Petitions
Mail Stop Petition
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING UNDER 37 CFR § 1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to the: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on **January 24, 2005**.

By: _____

Mary Ellen Waite

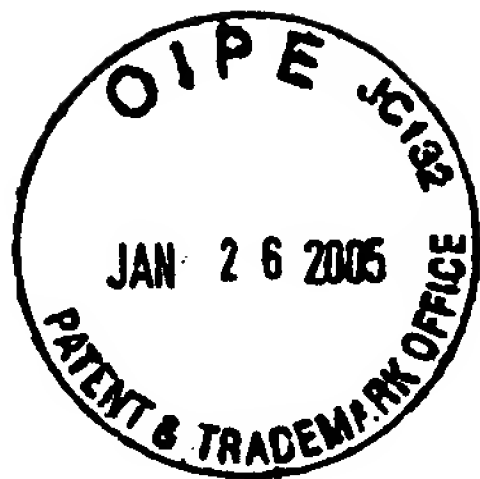
Sir or Madam:

Applicants submit for filing in the U.S. Patent and Trademark Office a Petition For Revival Of An Application For Patent Abandoned Unintentionally Under 37 C.F.R. 1.137(b) in the above-identified application. A check in the amount of \$750.00 is enclosed to cover the filing fee for such Petition.

The Commissioner is hereby authorized to charge any additional fee or credit overpayment to our Deposit Account No. 08-1290. **An originally executed duplicate of this transmittal is enclosed for this purpose.**

Dated: January 24, 2005

David A. Casimir
Registration No. 42,395
MEDLEN & CARROLL, LLP
101 Howard Street, Suite 305
San Francisco, California 94105
608/218-6900



PATENT
Attorney Docket No. **FORS-04447**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: **Michae W. Kaiser *et al.***

Serial No.: 09/684,305

Filed: 10/06/00

Entitled: **IMPROVED CLEAVAGE AGENTS**

Group No.: 1637

Examiner: JN Fredman

**AMENDMENT AND
SUBSTITUTE SEQUENCE LISTING**

MAIL STOP PETITION

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)

I hereby certify that this correspondence (along with any referred to as being attached or enclosed) is, on the date shown below, being deposited with the U.S. Postal Service with sufficient postage as first class mail in an envelope addressed to: MAIL STOP PETITION Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Dated: 1-24-05

By: 

Mary Ellen Waite

Sir or Madam:

Please amend the application as follows:

Amendment to the Specification begins on page 2 of this communication.

Remarks are on page 3 of this communication.


AMENDMENT TO THE SPECIFICATION

Please replace the Sequence Listing filed October 6, 2000 with the substitute Sequence Listing attached here as pages 1-124.

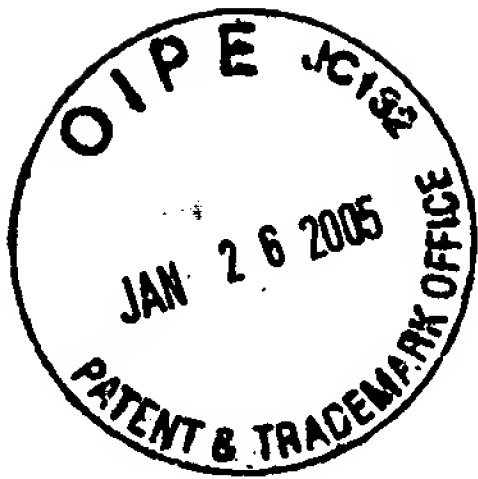
REMARKS

Applicants submit this substitute Sequence Listing to provide as a separate part of the disclosure, a "Sequence Listing" pursuant to 37 C.F.R §§1.821-1.825. In addition, Applicants submit herewith the substitute Sequence Listing in paper copy and on floppy disk in computer readable form. Applicants' amendments do not introduce new matter.

Dated: 1/24/05

By: 
David A. Casimir
Registration No. 42,395

MEDLEN & CARROLL, LLP
101 Howard Street, Suite 350
San Francisco, California 94105
415.904.6500



PATENT
Attorney Docket No. **FORS-04447**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: **Michael W. Kaiser *et al.***
Serial No.: **09/684,305**
Filed: **10/06/00**
Entitled: **IMPROVED CLEAVAGE AGENTS**
Group No.: **1637**
Examiner: **JN Fredman**

CERTIFICATE RE: SEQUENCE LISTING

MAIL STOP PETITION
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)	
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Dated: <u>1/24/05</u>	By: <u>Mary Ellen Waite</u> Mary Ellen Waite

Sir or Madam:

I hereby state that the enclosed Sequence Listing is being submitted in paper copy and on a computer-readable diskette, and that the content of the paper and computer readable copies are the same.

Dated: 1/24/05

By: David A. Casimir

David A. Casimir
Registration No. 42,395

MEDLEN & CARROLL, LLP
101 Howard Street, Suite 350
San Francisco, California 94105
415.904.6500



SEQUENCE LISTING

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Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	130	135	140
Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	145	150	155
Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	165	170	175
Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	180	185	190
Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	195	200	205
Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	210	215	220
Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	225	230	235
Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	245	250	255
Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe	260	265	270
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	275	280	285
Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	290	295	300
Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	305	310	315
Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	325	330	335
Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	340	345	350
Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	355	360	365
Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	370	375	380
Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	385	390	395
Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	405	410	415

Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu
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Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly
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Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala
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Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His
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Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp
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Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg
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Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile
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Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr
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His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser
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Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala
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Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr
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Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg
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Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
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Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
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Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
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Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala
785					790					795					800
Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
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Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	Tyr
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Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
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Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ala	Ile	Leu	His	Pro	Glu	Gly	Tyr
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Leu	Ile	Thr	Pro	Ala	Trp	Leu	Tyr	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu
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Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
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Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Gln	Arg	Leu	Ile	Arg		
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Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Phe	Gln	His	Leu	Asp	Gln	Val	Lys		
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Pro	Ser	Leu	Arg	Glu	Lys	Leu	Gln	Ala	Gly	Met	Glu	Ala	Leu	Ala	Leu		
225					230					235						240	
Ser	Arg	Lys	Leu	Ser	Gln	Val	His	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp		
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Phe	Gly	Arg	Arg	Arg	Thr	Pro	Asn	Leu	Glu	Gly	Leu	Arg	Ala	Phe	Leu		
			260					265					270				
Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu		
		275					280					285					
Gly	Pro	Lys	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala		
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Phe	Leu	Gly	Phe	Ser	Phe	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu		
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Leu	Ala	Leu	Ala	Gly	Ala	Trp	Glu	Gly	Arg	Leu	His	Arg	Ala	Gln	Asp		
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Pro	Leu	Arg	Gly	Leu	Arg	Asp	Leu	Lys	Gly	Val	Arg	Gly	Ile	Leu	Ala		
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Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp	Leu	Phe	Pro		
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Glu	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr		
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Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp		
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Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Phe	Gln	Thr	Leu	Lys		
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Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val		
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Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Glu	Ala		
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Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val		
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Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr	Tyr
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Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser
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Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg
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Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Val	Leu	Val	Val	Leu
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Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp
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Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln
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Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala
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Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu
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Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val
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Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val
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Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Arg	Leu	Phe
		755					760					765			
Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp
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785					790					795					800
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu
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Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
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Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
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Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
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Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
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Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
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Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
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Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
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Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
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Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Pro	Glu	Pro	Met	Trp 320
Ala	Glu	Leu	Lys	Ala 325	Leu	Ala	Ala	Cys	Arg 330	Asp	Gly	Arg	Val	His 335	Arg
Ala	Ala	Asp	Pro 340	Leu	Ala	Gly	Leu	Lys 345	Asp	Leu	Lys	Glu	Val 350	Arg	Gly
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Leu 370	Val	Pro	Gly	Asp	Asp	Pro	Met 375	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg	Arg 395	Tyr	Gly	Gly	Glu	Trp 400
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg
Asn	Leu	Leu	Lys 420	Arg	Leu	Glu	Gly 425	Glu	Glu	Lys	Leu	Leu	Trp 430	Leu	Tyr
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala
Thr 450	Gly	Val	Arg	Leu	Asp	Val 455	Ala	Tyr	Leu	Gln	Ala 460	Leu	Ser	Leu	Glu
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu 475	Val	Phe	Arg	Leu	Ala 480
Gly	His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp 490	Gln	Leu	Glu	Arg	Val 495	Leu
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala 505	Leu	Gly	Lys	Thr	Gln	Lys 510	Thr	Gly
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His
Pro 530	Ile	Val	Glu	Lys	Ile	Leu 535	Gln	His	Arg	Glu	Leu 540	Thr	Lys	Leu	Lys
Asn 545	Thr	Tyr	Val	Asp	Pro 550	Leu	Pro	Ser	Leu	Val 555	His	Pro	Arg	Thr	Gly 560
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Val 610	Ala	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu
Ser 625	Gly	Asp	Glu	Asn	Leu 630	Ile	Arg	Val	Phe	Gln 635	Glu	Gly	Lys	Asp	Ile 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
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 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
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 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
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 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
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Lys Gly

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 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1497)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1530)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1569)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1572)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1641)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1653)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1655)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1770)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1812)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (2319)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (2346)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (2396)
 <223> The n at this position can be a, c, t or g.

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 gtgcaggcgg tctacggctt cgccaagagc ctctcaagg ccctgaagga ggacggggac 180
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<210> 8
 <211> 833
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <220>
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 <222> (2)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (63)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (109)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (186)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (205)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (209)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (227)..(228)
 <223> Xaa at these positions can be any amino acid.

 <220>
 <221> SITE
 <222> (233)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (240)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (243)..(244)
 <223> Xaa at these positions can be any amino acid.

 <220>
 <221> SITE
 <222> (247)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (260)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (290)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (329)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (336)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (340)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (368)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (414)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (417)..(418)
 <223> Xaa at these positions can be any amino acid.

<220>
 <221> SITE
 <222> (431)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (551)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (605)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (773)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (794)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (798)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (823)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (833)
 <223> Xaa at this position can be any amino acid.

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 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
 20 25 30
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val
 50 55 60
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala
 65 70 75 80
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 85 90 95
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu
 100 105 110
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
 130 135 140
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175
 Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
 195 200 205
 Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
 210 215 220

Lys 225	Pro	Xaa	Xaa	Arg	Glu 230	Lys	Ile	Xaa	Ala	His 235	Met	Glu	Asp	Leu	Xaa 240
Leu	Ser	Xaa	Xaa	Leu 245	Ser	Xaa	Val	Arg	Thr 250	Asp	Leu	Pro	Leu	Glu 255	Val
Asp	Phe	Ala	Xaa 260	Arg	Arg	Glu	Pro	Asp 265	Arg	Glu	Gly	Leu	Arg 270	Ala	Phe
Leu	Glu	Arg 275	Leu	Glu	Phe	Gly	Ser 280	Leu	Leu	His	Glu	Phe 285	Gly	Leu	Leu
Glu 290	Xaa	Pro	Lys	Ala	Leu	Glu 295	Glu	Ala	Pro	Trp	Pro 300	Pro	Pro	Glu	Gly
Ala 305	Phe	Val	Gly	Phe	Val 310	Leu	Ser	Arg	Pro	Glu 315	Pro	Met	Trp	Ala	Glu 320
Leu	Leu	Ala	Leu	Ala 325	Ala	Ala	Arg	Xaa	Gly 330	Arg	Val	His	Arg	Ala 335	Xaa
Asp	Pro	Leu	Xaa 340	Gly	Leu	Arg	Asp	Leu 345	Lys	Glu	Val	Arg	Gly 350	Leu	Leu
Ala	Lys	Asp 355	Leu	Ala	Val	Leu	Ala 360	Leu	Arg	Glu	Gly	Leu 365	Asp	Leu	Xaa
Pro	Gly 370	Asp	Asp	Pro	Met	Leu 375	Leu	Ala	Tyr	Leu	Leu 380	Asp	Pro	Ser	Asn
Thr 385	Thr	Pro	Glu	Gly	Val 390	Ala	Arg	Arg	Tyr	Gly 395	Gly	Glu	Trp	Thr	Glu 400
Asp	Ala	Gly	Glu	Arg 405	Ala	Leu	Leu	Ser	Glu 410	Arg	Leu	Phe	Xaa	Asn 415	Leu
Xaa	Xaa	Arg	Leu 420	Glu	Gly	Glu	Glu 425	Arg	Leu	Leu	Trp	Leu	Tyr 430	Xaa	Glu
Val	Glu	Lys 435	Pro	Leu	Ser	Arg	Val 440	Leu	Ala	His	Met	Glu 445	Ala	Thr	Gly
Val 450	Arg	Leu	Asp	Val	Ala	Tyr 455	Leu	Gln	Ala	Leu	Ser 460	Leu	Glu	Val	Ala
Glu 465	Glu	Ile	Arg	Arg	Leu 470	Glu	Glu	Glu	Val	Phe 475	Arg	Leu	Ala	Gly	His 480
Pro	Phe	Asn	Leu	Asn 485	Ser	Arg	Asp	Gln	Leu 490	Glu	Arg	Val	Leu	Phe 495	Asp
Glu	Leu	Gly	Leu 500	Pro	Ala	Ile	Gly	Lys 505	Thr	Glu	Lys	Thr	Gly 510	Lys	Arg
Ser	Thr	Ser 515	Ala	Ala	Val	Leu	Glu 520	Ala	Leu	Arg	Glu	Ala 525	His	Pro	Ile
Val 530	Glu	Lys	Ile	Leu	Gln	Tyr 535	Arg	Glu	Leu	Thr	Lys 540	Leu	Lys	Asn	Thr
Tyr 545	Ile	Asp	Pro	Leu	Pro 550	Xaa	Leu	Val	His	Pro 555	Arg	Thr	Gly	Arg	Leu 560

His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	
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Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	
			580					585					590			
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Xaa	Leu	Val	Ala	
		595					600					605				
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	
	610					615					620					
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	
625					630					635					640	
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro	
				645					650					655		
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	
			660					665					670			
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	
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Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	
	690					695					700					
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	
705					710					715					720	
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	
				725					730					735		
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	
			740					745					750			
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	
		755					760					765				
Phe	Pro	Arg	Leu	Xaa	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	
	770					775					780					
Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Xaa	Arg	Ala	Glu	Xaa	Val	Ala	
785					790					795					800	
Ala	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	
				805					810					815		
Leu	Glu	Val	Glu	Val	Gly	Xaa	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	
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Xaa

<210> 9

<211> 1647

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

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ccggtgcagg cggtctacgg ctccgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
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<210> 10
<211> 2088
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 10

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
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<210> 11

<211> 962

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

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tggccgtgcc cctggaggtg gaggtgggga taggggagga ctggctctcc gccaaaggag 960
ga 962

<210> 12
<211> 1600
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 12

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atggaattcg gggatgctgc ccctctttga gccaagggc cgggtcctcc tggtaggacgg 60
ccaccacctg gcctaccgca ccttccacgc cctgaagggc ctcaccacca gccgggggga 120
gccggtgcag gcggtctacg gcttcgccaa gagcctcctc aaggccctca aggaggacgg 180
ggacgcggtg atcgtggtct ttgacgccaa ggccccctcc ttccgccacg aggcctacgg 240
ggggtacaag gcgggcccgg ccccccacgc ggaggacttt ccccggaac tcgccctcat 300
caaggagctg gtggacctcc tggggctggc gcgcctcgag gtcccgggct acgaggcgga 360
cgacgtcctg gccagcctgg ccaagaaggc ggaaaaggag ggctacgagg tccgcctcct 420
caccgccgac aaagaccttt accagctcct ttccgaccgc atccacgtcc tccaccccga 480
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ggccgactac cgggccctga ccggggacga gtccgacaac ctcccgggg tcaagggcat 600
cggggagaag acggcgagga agcttctgga ggagtggggg agcctggaag ccctcctcaa 660
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gaagctctcc tgggacctgg ccaagggtgc caccgacctg cccctggagg tggacttcgc 780
caaaaggcgg gagcccgacc gggagaggct tagggccttt ctggagaggc ttgagtttgg 840
cagcctcctc cacgagttcg gccttctgga aagccccaag atccgccggg ccttcatcgc 900
cgaggagggg tggctattgg tggccctgga ctatagccag atagagctca gggtagctggc 960
ccacctctcc ggcgacgaga acctgatccg ggtcttccag gaggggaggg acatccacac 1020
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ccttcaggtc cacgacgagc tggtcctcga ggccccaaaa gagagggcgg aggccgtggc 1500
ccggctggcc aaggaggtca tggagggggg gtatcccctg gccgtgcccc tggaggtgga 1560
ggtaggggata ggggaggact ggctctccgc caaggagtga 1600
```

<210> 13
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 13
 cacgaattcg gggatgctgc ccctctttga gcccaa 36

 <210> 14
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 14
 gtgagatcta tcactccttg gcggagagcc agtc 34

 <210> 15
 <211> 91
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 15
 taatacgact cactataggg agaccggaat tcgagctcgc ccgggcgagc tcgaattccg 60
 tgtattctat agtgtcacct aaatcgaatt c 91

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 16
 taatacgact cactataggg 20

 <210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 17
 gaattcgatt taggtgacac tatagaa 27

<210> 18
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 18
 gtaatcatgg tcatagctgg tagcttgcta c 31

 <210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 19
 ggatcctcta gagtcgacct gcaggcatgc ctaccttggt ag 42

 <210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 20
 ggatcctcta gagtcgacct gcaggcatgc 30

 <210> 21
 <211> 2502
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 21
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
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 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacgccc gaggaacttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 gggtagctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccgggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcg cccgacctgc ccctggagggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840
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 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gaggcttctg 1080
 gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgcctacctc 1140
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 cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620
 aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680
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 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgcgggcca ccgcctctcc 2040
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 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccggggcac cgccgcccgc 2280
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340
 ctcttcagg tccacgacga gctggtcctc gaggcccaaa aagagagggc ggaggccgtg 2400

gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460
gaggtgggga taggggagga ctggctctcc gcccaaggagt ga 2502

<210> 22
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 22
gatttaggtg acactatag 19

<210> 23
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 23
cggacgaaca agcgagacag cgacacaggt accacatggt acaagaggca agagagacga 60
cacagcagaa ac 72

<210> 24
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 24
gtttctgctg tgtcgtctct cttgcctctt gtaccatgtg gtacctgtgt cgctgtctcg 60
cttgttcgtc 70

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 25
gacgaacaag cgagacagcg 20

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 26
 gtttctgctg tgcgtctct cttg 24

 <210> 27
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 27
 cctcttgtag catgtggtac ctgtgtcgct gtctcgcttg ttcgtc 46

 <210> 28
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 28
 acacaggtac cacatggtac aagaggcaag agagacgaca cagcagaaac 50

 <210> 29
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 29
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser
 1 5 10 15

 <210> 30
 <211> 969
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 30
 atggctagca tgactggtgg acagcaaagt ggtcggatca attcggggat gctgccctc 60
 tttgagccca agggccgggt cctcctggtg gacggccacc acctggccta ccgcaccttc 120

cacgccctga agggcctcac caccagccgg ggggagccgg tgcaggcggt ctacggcttc 180
 gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggtgatcgt ggtctttgac 240
 gccaaggccc cctccttccg ccacgaggcc tacgggggggt acaaggcggg ccgggcccc 300
 acgccggagg actttccccg gcaactcgcc ctcatcaagg agctgggtgga cctcctgggg 360
 ctggcgcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420
 aaggcggaaa aggagggcta cgaggtccgc atcctcaccg ccgacaaaga cctttaccag 480
 cttctttccg accgcatcca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540
 ctttgggaaa agtacggcct gaggcccgac cagtgggccc actaccgggc cctgaccggg 600
 gacgagtccg acaaccttcc cgggggtcaag ggcacgggg agaagacggc gaggaagctt 660
 ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagcccgcc 720
 atccgggaga agatcctggc ccacatggac gatctgaagc tctcctggga cctggccaag 780
 gtgcgccacc acctgcccct ggaggtggac ttgcgcaaaa ggcgggagcc cgaccgggag 840
 aggcttaggg cctttctgga gaggttgag ttggcagcc tcctccacga gttcggcctt 900
 ctggaaagcc ccaagtcatg gaggggggtgt atcccctggc cgtgcccctg gaggtggagg 960
 tggggatag 969

<210> 31
 <211> 948
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 31
 atggctagca tgactggtgg acagcaaata ggtcggatca attcggggat gctgcccctc 60
 tttgagccca agggccgggt cctcctgggt gacggccacc acctggccta ccgcaccttc 120
 cacgccctga agggcctcac caccagccgg ggggagccgg tgcaggcggt ctacggcttc 180
 gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggtgatcgt ggtctttgac 240
 gccaaggccc cctccttccg ccacgaggcc tacgggggggt acaaggcggg ccgggcccc 300
 acgccggagg actttccccg gcaactcgcc ctcatcaagg agctgggtgga cctcctgggg 360
 ctggcgcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420
 aaggcggaaa aggagggcta cgaggtccgc atcctcaccg ccgacaaaga cctttaccag 480
 cttctttccg accgcatcca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540
 ctttgggaaa agtacggcct gaggcccgac cagtgggccc actaccgggc cctgaccggg 600
 gacgagtccg acaaccttcc cgggggtcaag ggcacgggg agaagacggc gaggaagctt 660

ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagcccgcc 720
atccgggaga agatcctggc ccacatggac gatctgaagc tctcctggga cctggccaag 780
gtgcgcaccg acctgcccct ggaggtggac ttcgccaaaa ggcgggagcc cgaccgggag 840
aggcttaggg cctttctgga gaggttgag tttggcagcc tcctccacga gttcggcctt 900
ctggaaagcc ccaaggccgc actcgagcac caccaccacc accactga 948

<210> 32
<211> 206
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 32
cgccagggtt ttcccagtca cgacgttgta aaacgacggc cagtgaattg taatacgact 60
cactataggg cgaattcgag ctcggtaccc ggggatcctc tagagtcgac ctgcaggcat 120
gcaagcttga gtattctata gtgtcaccta aatagcttgg cgtaatcatg gtcatacttg 180
tttctgtgtg gaaattgtta tccgct 206

<210> 33
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 33
ttctgggttc tctgctctct ggtcgctgtc tcgcttggtc gtc 43

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 34
gctgtctcgc ttgttcgtc 19

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 35
 gacgaacaag cgagacagcg 20

<210> 36
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 36
 ttctgggttc tctgctctct ggtc 24

<210> 37
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 37
 gacgaacaag cgagacagcg accagagagc agagaaccca gaa 43

<210> 38
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 38
 accagagagc agagaaccca gaa 23

<210> 39
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 39
 aacagctatg accatgatta c 21

<210> 40
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 40
 gttctctgct ctctggtcgc tgtctcgctt gtgaaacaag cgagacagcg tggctctctcg 60

<210> 41
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 41
 cgagagacca cgctg 15

<210> 42
 <211> 52
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 42
 cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gctttccccg tc 52

<210> 43
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 43
 agaaaggaag ggaagaaagc gaaagg 26

<210> 44
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 44
 gacggggaaa gccggcgaac g 21

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 45
 gaaagccggc gaacgtggcg 20

<210> 46
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 46
 ggcgaacgtg gcgagaaagg a 21

 <210> 47
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 47
 cctttcgctt tcttccttc ctttctgcc acgttcgccg gc 42

 <210> 48
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 48
 cctttcgctc tcttccttc ctttctgcc acgttcgccg gc 42

 <210> 49
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (8)
 <223> The A residue at this position is
 2'-O-methyladenosine.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 49
 agaaaggaag ggaagaaagc gaaaggt 27

 <210> 50
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

<400> 50 gccggcggaac gtggcgagaa agga	24
<210> 51 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 51 ggtttttctt tgaggtttag	20
<210> 52 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 52 gcgacactcc accatagat	19
<210> 53 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 53 ctgtcttcac gcagaaagc	19
<210> 54 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 54 gcacggtcta cgagacctc	19
<210> 55 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 55 taatacgact cactataggg	20

<210> 56
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 56
gggaaagcuu gcaugccugc aggucgacuc uagaggaucau acuagucaua uggauucugu 60
cuucacgcag aaagcgucug gccaugggcu uaguaugagu gucgugcagc cuccaggacc 120
ccccucuccg ggagaggcau aguggucugc ggaaccggug aguacaccgg aauugccagg 180
acgaccgggu ccuuucuugg auaaaccgc ucaaugccug gagauuuggg cgugcccccg 240
caagacugcu agccgaguag uguugggucg cgaaaggccu ugugguacug ccugauaggg 300
ugccugcgag ugccccggga ggucucguag accgugc 337

<210> 57
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<220>
<221> misc_feature
<222> (17)
<223> The T at this position is linked to a fluorescein
dye on an abasic linker.

<400> 57
ccggtcgtcc tggcaatcc 19

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 58
gtttatccaa gaaaggaccc ggtc 24

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 59
 cagggtgaag ggaagaagaa agcgaaaggt 30

<210> 60
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 60
 cagggggaag ggaagaagaa agcgaaaggt 30

<210> 61
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The T residues at positions 1 and 2 are amino modified T residues.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 61
 ttcttttcac cagcgagacg gg 22

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 62
 attgggcgcc aggggtggttt tt 22

<210> 63
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 63
 cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca atacgcaaac cgc 53

<210> 64
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 64
 gaattcgatt taggtgacac tatagaatac a 31

<210> 65
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 65
 cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gc 42

<210> 66
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 66
 gccggcgaac gtggcgagaa agga 24

<210> 67
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 67
 cagaaggaag ggaagaaagc gaaagg 26

<210> 68
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 68
 cagggggaag ggaagaaagc gaaagg 26

<210> 69
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 69
 cagggtacag ggaagaaagc gaaagg 26

<210> 70
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (24)
 <223> The residue at this position is a dideoxycytidine.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 70
 gccggcgaac gtggcgagaa aggc 24

<210> 71
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <220>
 <221> misc_feature
 <222> (26)
 <223> The G at this position is linked to a spacer
 bearing a Cy3 amidite group.

 <220>
 <221> misc_feature
 <222> (27)
 <223> The residue at this position is a dideoxycytidine.

 <400> 71
 agaaaggaag ggaagaaagc gaaaggc 27

<210> 72
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (1)
 <223> The A at this position is linked to a spacer
 containing a fluorescein label.

<220>
 <221> misc_feature
 <222> (26)
 <223> The G at this position is linked to a spacer
 bearing a Cy3 amidite group.

<220>
 <221> misc_feature
 <222> (27)
 <223> The residue at this position is a dideoxycytidine.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 72
 agaaaggaag ggaagaaagc gaaaggc 27

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The A at this position is linked to a spacer
 containing a fluorescein label.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 73
 agaaaggaag ggaagaaagc gaaagg 26

<210> 74
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The A at this position is linked to a spacer
 bearing a Cy3 amidite group.

<220>
 <221> misc_feature
 <222> (26)
 <223> The G at this position is linked to a spacer
 bearing a biotin group.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 74
 agaaaggaag ggaagaaagc gaaagg 27

<210> 75
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 75
 ggaaagccgg cgaacgtggc gaga 24

<210> 76
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 76
 ggaaagccgg cgaacgtggc gagaaa 26

<210> 77
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (1)
 <223> The T at this position is linked to a spacer
 bearing a Cy3 amidite group.

 <220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The residues at these positions have an amino
 group added.

 <220>
 <221> misc_feature
 <222> (22)
 <223> The T at this position is linked to a spacer
 containing a fluorescein label.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 77
 ttccagagcc taatttgcca gta 23

<210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position has a 5' TET-label.

<220>
 <221> misc_feature
 <222> (22)
 <223> The T at this position is linked to a spacer
 containing a fluorescein label.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 78
 ttccagagcc taatttgcca gta 23

<210> 79
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 79
 cttaccaacg ctaacgagcg tcttg 25

<210> 80
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (14)
 <223> The residue at this positions contain an abasic
 ribose.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 80
 cgagagacca cgct 14

<210> 81
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (14)
 <223> The residue at this position contains an abasic
 ribose with a 3' phosphate group.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 81
cgagagacca cgct 14

<210> 82
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (15)
<223> The residue at this position contains a 3'
phosphop group.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 82
cgagagacca cgctg 15

<210> 83
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 83
cccgtctcgc tgggtgaaaag aaaaaccacc ctggcgccca .ata 43

<210> 84
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (15)
<223> The G at this position is linked to a
3-nitropyrrole.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 84
tattgggcgc cagggggttt tt 22

<210> 85
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (15)
<223> The G at this position is linked to a
3-nitropyrrole group.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 85
 tattggg'gcgc catgggggttt tt 22

<210> 86
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 86
 tattggg'gcgc catggtgggtt ttt 23

<210> 87
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (9)
 <223> The G at this position is linked to a
 5-nitroindole.

<220>
 <221> misc_feature
 <222> (14)
 <223> The G at this position is linked to a
 5-nitroindole.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 87
 tattggg'gcgc aggggggtttt t 21

<210> 88
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (9)
 <223> The G at this position is linked to a
 5-nitroindole.

<220>
 <221> misc_feature
 <222> (14)
 <223> The G at this position is linked to a
 5-nitroindole.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 88
tattgggcgc atggggtttt t

21

<210> 89
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The T at this position is linked to a spacer
bearing a Cy3 amidite label.

<220>
<221> misc_feature
<222> (2)..(3)
<223> The residues at these positions have an amino
group added.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 89
ttcaccag

8

<210> 90
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxyguanosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (4)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (5)..(6)
<223> The residues at these positions are
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (7)..(8)
<223> The residues at these positions are
2'deoxyguanosine 5'-O-(1-Thiomonophosphate)

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 90
gctcaaggca ctcttgacct cga

23

<210> 91
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)..(4)
<223> The residues at these positions are a
2'deoxycytosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (5)..(6)
<223> The residues at these positions are a
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (7)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (8)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxyadenosine
5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 91
ctccaactac cacaagttta tattcag

27

<210> 92
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxyguanosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (4)..(5)
<223> The residues at these positions are a
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (6)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (7)
<223> The residue at this position is a 2'deoxyadenosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (8)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (9)..(10)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 92
 ctgaatataa acttgtggta gttggagctg gtgacgtagg caagagtgcc ttgacg 56

<210> 93
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position is a 2'deoxycytosine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (2)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (3)
 <223> The residue at this position is a 2'deoxyguanosine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (4)..(5)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (6)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (7)
 <223> The residue at this position is a 2'deoxyadenosine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (8)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (9)..(10)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate) .

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 93
 ctgaatataa acttgtggta gttggagctg gtgccgtagg caagagtgcc ttgacg 56

<210> 94
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position has a TET label.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 94
 ccggtcgtcc tggcaa 16

<210> 95
 <211> 13
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position has a TET label.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 95
 ccggtcgtcc tgg 13

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 96
 caattccggt gtactcacg gttcc 25

<210> 97
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The T at this position is linked to a spacer
bearing a Cy3 amidite label.

<220>
<221> misc_feature
<222> (2)..(3)
<223> The residues at these positions have an amino
group added.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 97
ttccagag

8

<210> 98
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxyguanosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)..(4)
<223> The residues at these positions are a
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (5)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (6)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (7)..(8)
 <223> The residues at these positions are a
 2'deoxythymidine 5'-O-(1-Thiomonophosphate) .

<220>
 <221> misc_feature
 <222> (9)
 <223> The residue at this position is a 2'deoxyadenosine
 5'-O-(1-Thiomonophosphate) .

<220>
 <221> misc_feature
 <222> (10)
 <223> The residue at this position is a 2'deoxycytosine
 5'-O-(1-Thiomonophosphate) .

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 98
 gtaatcttac caacgctaac gagcgtcttg

<210> 99
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The residues at these positions are a
 2'deoxyctosine 5'-O-(1-Thiomonophosphate) .

<220>
 <221> misc_feature
 <222> (3)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate) .

<220>
 <221> misc_feature
 <222> (4)..(5)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate) .

<220>
 <221> misc_feature
 <222> (6)..(8)
 <223> The residues at these positions are a
 2'deoxythymidine 5'-O-(1-Thiomonophosphate) .

<220>
 <221> misc_feature
 <222> (9)
 <223> The residue at this position is a 2'deoxyguanosine
 5'-O-(1-Thiomonophosphate) .

30

<220>
 <221> misc_feature
 <222> (10)
 <223> The residue at this position is a 2'deoxyctosine
 5'-O-(1-Thiomonophosphate) .

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 99
 cctaatttgc cagttacaaa ataaacagcc 30

<210> 100
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 100
 gggaaagtcc tcggagccgc gcgggacgag cgtggggggcc cg 42

<210> 101
 <211> 963
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<220>
 <221> CDS
 <222> (1)..(960)

<400> 101
 atg gct agc atg act ggt gga cag caa atg ggt cgg atc aat tcg ggg 48
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
 1 5 10 15
 atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc ctg gtg gac ggc 96
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
 20 25 30
 cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag ggc ctc acc acc 144
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
 35 40 45
 agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc gcc aag agc ctc 192
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
 50 55 60
 ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc gtg gtc ttt gac 240
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
 65 70 75 80
 gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg ggg tac aag gcg 288
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
 85 90 95

ggc	cgg	gcc	ccc	acg	ctc	gtc	ccg	cgc	ggc	tcc	gag	gac	ttt	ccc	cgg	336
Gly	Arg	Ala	Pro	Thr	Leu	Val	Pro	Arg	Gly	Ser	Glu	Asp	Phe	Pro	Arg	
			100					105					110			
caa	ctc	gcc	ctc	atc	aag	gag	ctg	gtg	gac	ctc	ctg	ggg	ctg	gcg	cgc	384
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	
		115					120					125				
ctc	gag	gtc	ccg	ggc	tac	gag	gcg	gac	gac	gtc	ctg	gcc	agc	ctg	gcc	432
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	
	130					135					140					
aag	aag	gcg	gaa	aag	gag	ggc	tac	gag	gtc	cgc	atc	ctc	acc	gcc	gac	480
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	
145					150					155					160	
aaa	gac	ctt	tac	cag	ctc	ctt	tcc	gac	cgc	atc	cac	gtc	ctc	cac	ccc	528
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	
				165					170					175		
gag	ggg	tac	ctc	atc	acc	ccg	gcc	tgg	ctt	tgg	gaa	aag	tac	ggc	ctg	576
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	
			180					185					190			
agg	ccc	gac	cag	tgg	gcc	gac	tac	cgg	gcc	ctg	acc	ggg	gac	gag	tcc	624
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	
		195					200					205				
gac	aac	ctt	ccc	ggg	gtc	aag	ggc	atc	ggg	gag	aag	acg	gcg	agg	aag	672
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	
	210					215					220					
ctt	ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac	720
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	
225					230					235					240	
cgg	ctg	aag	ccc	gcc	atc	cgg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat	768
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	
				245					250					255		
ctg	aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	cgc	acc	gac	ctg	ccc	ctg	816
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	
			260					265					270			
gag	gtg	gac	ttc	gcc	aaa	agg	cgg	gag	ccc	gac	cgg	gag	agg	ctt	agg	864
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	
		275					280					285				
gcc	ttt	ctg	gag	agg	ctt	gag	ttt	ggc	agc	ctc	ctc	cac	gag	ttc	ggc	912
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	
	290					295					300					
ctt	ctg	gaa	agc	ccc	aag	gcc	gca	ctc	gag	cac	cac	cac	cac	cac	cac	960
Leu	Leu	Glu	Ser	Pro	Lys	Ala	Ala	Leu	Glu	His	His	His	His	His	His	
305					310					315					320	
tga																963

<210> 102
 <211> 320
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 102

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Ile	Asn	Ser	Gly
1				5					10					15	
Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
			20					25					30		
His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	Thr	Thr
		35					40					45			
Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu
	50					55					60				
Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	Phe	Asp
65					70					75					80
Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr	Lys	Ala
				85					90					95	
Gly	Arg	Ala	Pro	Thr	Leu	Val	Pro	Arg	Gly	Ser	Glu	Asp	Phe	Pro	Arg
			100					105					110		
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg
		115					120					125			
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala
	130					135					140				
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp
145					150					155					160
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro
				165					170					175	
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu
			180					185					190		
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser
		195					200					205			
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys
	210					215					220				
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp
225					230					235					240
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp
				245					250					255	
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu
			260					265					270		
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg
		275					280					285			

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
290 295 300

Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His
305 310 315 320

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 103
cgatctcctc ggccacctcc 20

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 104
ggcggtgccc tggacgggca 20

<210> 105
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 105
ccagctcggt gtggacctga 20

<210> 106
<211> 2505
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(2499)

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 106
atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

ctg	gtg	gac	ggc	cac	cac	ctg	gcc	tac	cgc	acc	ttc	cac	gcc	ctg	aag	96
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	
			20					25					30			
ggc	ctc	acc	acc	agc	cgg	ggg	gag	ccg	gtg	cag	gcg	gtc	tac	ggc	ttc	144
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	
		35					40					45				
gcc	aag	agc	ctc	ctc	aag	gcc	ctc	aag	gag	gac	ggg	gac	gcg	gtg	atc	192
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	
	50					55					60					
gtg	gtc	ttt	gac	gcc	aag	gcc	ccc	tcc	ttc	cgc	cac	gag	gcc	tac	ggg	240
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	
	65				70					75					80	
ggg	tac	aag	gcg	ggc	cgg	gcc	ccc	acg	ccg	gag	gac	ttt	ccc	cgg	caa	288
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	
				85				90					95			
ctc	gcc	ctc	atc	aag	gag	ctg	gtg	gac	ctc	ctg	ggg	ctg	gcg	cgc	ctc	336
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	
			100					105					110			
gag	gtc	ccg	ggc	tac	gag	gcg	gac	gac	gtc	ctg	gcc	agc	ctg	gcc	aag	384
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	
		115					120					125				
aag	gcg	gaa	aag	gag	ggc	tac	gag	gtc	cgc	atc	ctc	acc	gcc	gac	aaa	432
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	
	130					135					140					
gac	ctt	tac	cag	ctc	ctt	tcc	gac	cgc	atc	cac	gtc	ctc	cac	ccc	gag	480
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	
	145				150					155					160	
ggg	tac	ctc	atc	acc	ccg	gcc	tgg	ctt	tgg	gaa	aag	tac	ggc	ctg	agg	528
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	
				165				170						175		
ccc	gac	cag	tgg	gcc	gac	tac	cgg	gcc	ctg	acc	ggg	gac	gag	tcc	gac	576
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
			180					185					190			
aac	ctt	ccc	ggg	gtc	aag	ggc	atc	ggg	gag	aag	acg	gcg	agg	aag	ctt	624
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	
		195					200					205				
ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac	cgg	672
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
ctg	aag	ccc	gcc	atc	cgg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat	ctg	720
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	
	225				230					235					240	
aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	cgc	acc	gac	ctg	ccc	ctg	gag	768
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	
				245					250					255		

gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	816
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	864
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	912
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	960
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	1008
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	1056
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	1104
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	1152
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	1200
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	1248
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	1296
420 425 430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	1344
435 440 445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	1392
450 455 460	
gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly	1440
465 470 475 480	
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe	1488
485 490 495	

gac Asp	gag Glu	cta Leu	ggg Gly 500	ctt Leu	ccc Pro	gcc Ala	atc Ile	ggc Gly 505	aag Lys	acg Thr	gag Glu	aag Lys	acc Thr 510	ggc Gly	aag Lys	1536
cgc Arg	tcc Ser	acc Thr 515	agc Ser	gcc Ala	gcc Ala	gtc Val	ctg Leu 520	gag Glu	gcc Ala	ctc Leu	cgc Arg	gag Glu 525	gcc Ala	cac His	ccc Pro	1584
atc Ile	gtg Val 530	gag Glu	aag Lys	atc Ile	ctg Leu	cag Gln 535	tac Tyr	cgg Arg	gag Glu	ctc Leu	acc Thr 540	aag Lys	ctg Leu	aag Lys	agc Ser	1632
acc Thr 545	tac Tyr	att Ile	gac Asp	ccc Pro	ttg Leu 550	ccg Pro	gac Asp	ctc Leu	atc Ile	cac His 555	ccc Pro	agg Arg	acg Thr	ggc Gly	cgc Arg 560	1680
ctc Leu	cac His	acc Thr	cgc Arg	ttc Phe 565	aac Asn	cag Gln	acg Thr	gcc Ala 570	acg Thr	gcc Ala	acg Thr	ggc Gly	agg Arg	cta Leu 575	agt Ser	1728
agc Ser	tcc Ser	gat Asp	ccc Pro 580	aac Asn	ctc Leu	cag Gln	aac Asn	atc Ile 585	ccc Pro	gtc Val	cgc Arg	acc Thr	ccg Pro 590	ctt Leu	ggg Gly	1776
cag Gln	agg Arg	atc Ile 595	cgc Arg	cgg Arg	gcc Ala	ttc Phe	atc Ile 600	gcc Ala	gag Glu	gag Glu	ggg Gly	tgg Trp 605	cta Leu	ttg Leu	gtg Val	1824
gcc Ala 610	ctg Leu	gac Asp	tat Tyr	agc Ser	cag Gln	ata Ile 615	gag Glu	ctc Leu	agg Arg	gtg Val	ctg Leu 620	gcc Ala	cac His	ctc Leu	tcc Ser	1872
ggc Gly 625	gac Asp	gag Glu	aac Asn	ctg Leu	atc Ile 630	cgg Arg	gtc Val	ttc Phe	cag Gln	gag Glu 635	ggg Gly	cgg Arg	gac Asp	atc Ile	cac His 640	1920
acg Thr	gag Glu	acc Thr	gcc Ala	agc Ser 645	tgg Trp	atg Met	ttc Phe	ggc Gly	gtc Val 650	ccc Pro	cgg Arg	gag Glu	gcc Ala	gtg Val 655	gac Asp	1968
ccc Pro	ctg Leu	atg Met	cgc Arg 660	cgg Arg	gcg Ala	gcc Ala	aag Lys	acc Thr 665	atc Ile	aac Asn	ttc Phe	ggg Gly	gtc Val 670	ctc Leu	tac Tyr	2016
ggc Gly	atg Met	tcg Ser 675	gcc Ala	cac His	cgc Arg	ctc Leu	tcc Ser 680	cag Gln	gag Glu	cta Leu	gcc Ala	atc Ile 685	cct Pro	tac Tyr	gag Glu	2064
gag Glu 690	gcc Ala	cag Gln	gcc Ala	ttc Phe	att Ile	gag Glu 695	cgc Arg	tac Tyr	ttt Phe	cag Gln	agc Ser 700	ttc Phe	ccc Pro	aag Lys	gtg Val	2112
cgg Arg 705	gcc Ala	tgg Trp	att Ile	gag Glu	aag Lys 710	acc Thr	ctg Leu	gag Glu	gag Glu	ggc Gly 715	agg Arg	agg Arg	cgg Arg	ggg Gly	tac Tyr 720	2160
gtg Val	gag Glu	acc Thr	ctc Leu	ttc Phe 725	ggc Gly	cgc Arg	cgc Arg	cgc Arg	tac Tyr 730	gtg Val	cca Pro	gac Asp	cta Leu	gag Glu 735	gcc Ala	2208

cgg	gtg	aag	agc	gtg	cgg	gag	gcg	gcc	gag	cgc	atg	gcc	ttc	aac	atg	2256
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	
			740					745					750			
ccc	gtc	cag	ggc	acc	gcc	gcc	gac	ctc	atg	aag	ctg	gct	atg	gtg	aag	2304
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	
		755					760					765				
ctc	ttc	ccc	agg	ctg	gag	gaa	atg	ggg	gcc	agg	atg	ctc	ctt	cag	gtc	2352
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	
	770					775					780					
cac	aac	gag	ctg	gtc	ctc	gag	gcc	cca	aaa	gag	agg	gcg	gag	gcc	gtg	2400
His	Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	
	785				790					795					800	
gcc	cgg	ctg	gcc	aag	gag	gtc	atg	gag	ggg	gtg	tat	ccc	ctg	gcc	gtg	2448
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	
				805					810					815		
ccc	ctg	gag	gtg	gag	gtg	ggg	ata	ggg	gag	gac	tgg	ctc	tcc	gcc	aag	2496
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	
			820					825					830			
gag	tgatag															2505
Glu																

<210> 107
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 107
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	325	330	335
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	340	345	350
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	355	360	365
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	370	375	380
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	405	410	415
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	420	425	430
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460

Ala 465	Glu	Glu	Ile	Ala	Arg 470	Leu	Glu	Ala	Glu	Val 475	Phe	Arg	Leu	Ala	Gly 480
His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp	Gln 490	Leu	Glu	Arg	Val	Leu	Phe 495
Asp	Glu	Leu	Gly 500	Leu	Pro	Ala	Ile	Gly 505	Lys	Thr	Glu	Lys	Thr 510	Gly	Lys
Arg	Ser	Thr 515	Ser	Ala	Ala	Val	Leu 520	Glu	Ala	Leu	Arg	Glu 525	Ala	His	Pro
Ile 530	Val	Glu	Lys	Ile	Leu	Gln 535	Tyr	Arg	Glu	Leu	Thr 540	Lys	Leu	Lys	Ser
Thr 545	Tyr	Ile	Asp	Pro	Leu 550	Pro	Asp	Leu	Ile	His 555	Pro	Arg	Thr	Gly	Arg 560
Leu	His	Thr	Arg	Phe 565	Asn	Gln	Thr	Ala	Thr 570	Ala	Thr	Gly	Arg	Leu	Ser 575
Ser	Ser	Asp	Pro 580	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr	Pro 590	Leu	Gly
Gln	Arg	Ile 595	Arg	Arg	Ala	Phe	Ile 600	Ala	Glu	Glu	Gly	Trp 605	Leu	Leu	Val
Ala 610	Leu	Asp	Tyr	Ser	Gln	Ile 615	Glu	Leu	Arg	Val	Leu 620	Ala	His	Leu	Ser
Gly 625	Asp	Glu	Asn	Leu	Ile 630	Arg	Val	Phe	Gln	Glu 635	Gly	Arg	Asp	Ile	His 640
Thr	Glu	Thr	Ala	Ser 645	Trp	Met	Phe	Gly	Val 650	Pro	Arg	Glu	Ala	Val	Asp 655
Pro	Leu	Met	Arg 660	Arg	Ala	Ala	Lys	Thr 665	Ile	Asn	Phe	Gly	Val 670	Leu	Tyr
Gly	Met	Ser 675	Ala	His	Arg	Leu	Ser 680	Gln	Glu	Leu	Ala	Ile 685	Pro	Tyr	Glu
Glu 690	Ala	Gln	Ala	Phe	Ile	Glu 695	Arg	Tyr	Phe	Gln	Ser 700	Phe	Pro	Lys	Val
Arg 705	Ala	Trp	Ile	Glu	Lys 710	Thr	Leu	Glu	Glu	Gly 715	Arg	Arg	Arg	Gly	Tyr 720
Val	Glu	Thr	Leu	Phe 725	Gly	Arg	Arg	Arg	Tyr 730	Val	Pro	Asp	Leu	Glu	Ala 735
Arg	Val	Lys	Ser 740	Val	Arg	Glu	Ala	Ala 745	Glu	Arg	Met	Ala	Phe	Asn	Met 750
Pro	Val	Gln	Gly 755	Thr	Ala	Ala	Asp 760	Leu	Met	Lys	Leu	Ala 765	Met	Val	Lys
Leu 770	Phe	Pro	Arg	Leu	Glu	Glu 775	Met	Gly	Ala	Arg	Met 780	Leu	Leu	Gln	Val
His 785	Asn	Glu	Leu	Val	Leu 790	Glu	Ala	Pro	Lys	Glu 795	Arg	Ala	Glu	Ala	Val 800

Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	
				805					810					815		
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	
			820					825					830			
Glu																
<210> 108																
<211> 25																
<212> DNA																
<213> Artificial Sequence																
<220>																
<223> Description of Artificial Sequence: Synthetic																
<400> 108																
gggataccat gggagtgcag tttgg																25
<210> 109																
<211> 27																
<212> DNA																
<213> Artificial Sequence																
<220>																
<223> Description of Artificial Sequence: Synthetic																
<400> 109																
ggtaaatttt tctcgtcgac atccac																27
<210> 110																
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<212> DNA																
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<220>																
<221> CDS																
<222> (1)..(978)																
<400> 110																
atg	gga	gtg	cag	ttt	ggt	gat	ttt	att	cca	aaa	aat	att	atc	tcc	ttt	48
Met	Gly	Val	Gln	Phe	Gly	Asp	Phe	Ile	Pro	Lys	Asn	Ile	Ile	Ser	Phe	
1				5					10					15		
gaa	gat	tta	aaa	ggg	aaa	aaa	gta	gct	att	gat	gga	atg	aat	gca	tta	96
Glu	Asp	Leu	Lys	Gly	Lys	Lys	Val	Ala	Ile	Asp	Gly	Met	Asn	Ala	Leu	
			20					25					30			
tat	cag	ttt	tta	aca	tct	ata	cgt	ttg	aga	gat	ggt	tct	cca	ttg	aga	144
Tyr	Gln	Phe	Leu	Thr	Ser	Ile	Arg	Leu	Arg	Asp	Gly	Ser	Pro	Leu	Arg	
		35					40					45				
aat	aga	aaa	gga	gag	ata	acc	tca	gca	tat	aac	gga	gtt	ttt	tat	aaa	192
Asn	Arg	Lys	Gly	Glu	Ile	Thr	Ser	Ala	Tyr	Asn	Gly	Val	Phe	Tyr	Lys	
		50				55					60					

acc Thr 65	ata Ile	cat His	ttg Leu	tta Leu	gag Glu 70	aat Asn	gat Asp	ata Ile	act Thr	cca Pro 75	atc Ile	tgg Trp	gtt Val	ttt Phe 80	gat Asp	240
ggt Gly	gag Glu	cca Pro	cca Pro	aag Lys 85	tta Leu	aag Lys	gag Glu	aaa Lys	aca Thr 90	agg Arg	aaa Lys	gtt Val	agg Arg	aga Arg 95	gag Glu	288
atg Met	aaa Lys	gag Glu	aaa Lys 100	gct Ala	gaa Glu	ctt Leu	aag Lys	atg Met 105	aaa Lys	gag Glu	gca Ala	att Ile	aaa Lys 110	aag Lys	gag Glu	336
gat Asp	ttt Phe	gaa Glu 115	gaa Glu	gct Ala	gct Ala	aag Lys	tat Tyr 120	gca Ala	aag Lys	agg Arg	gtt Val	agc Ser 125	tat Tyr	cta Leu	act Thr	384
ccg Pro 130	aaa Lys	atg Met	gtt Val	gaa Glu	aac Asn	tgc Cys 135	aaa Lys	tat Tyr	ttg Leu	tta Leu	agt Ser 140	ttg Leu	atg Met	ggc Gly	att Ile	432
ccg Pro 145	tat Tyr	gtt Val	gaa Glu	gct Ala	ccc Pro 150	tct Ser	gag Glu	gga Gly	gag Glu	gca Ala 155	caa Gln	gca Ala	agc Ser	tat Tyr	atg Met 160	480
gca Ala	aag Lys	aag Lys	gga Gly	gat Asp 165	gtt Val	tgg Trp	gca Ala	gtt Val	gta Val 170	agt Ser	caa Gln	gat Asp	tat Tyr	gat Asp 175	gcc Ala	528
ttg Leu	tta Leu	tat Tyr	gga Gly 180	gct Ala	ccg Pro	aga Arg	gtt Val	gtt Val 185	aga Arg	aat Asn	tta Leu	aca Thr	act Thr 190	aca Thr	aag Lys	576
gag Glu	atg Met	cca Pro 195	gaa Glu	ctt Leu	att Ile	gaa Glu	tta Leu 200	aat Asn	gag Glu	gtt Val	tta Leu	gag Glu 205	gat Asp	tta Leu	aga Arg	624
att Ile 210	tct Ser	ttg Leu	gat Asp	gat Asp	ttg Leu	ata Ile 215	gat Asp	ata Ile	gcc Ala	ata Ile	ttt Phe 220	atg Met	gga Gly	act Thr	gac Asp	672
tat Tyr 225	aat Asn	cca Pro	gga Gly	gga Gly	gtt Val 230	aaa Lys	gga Gly	ata Ile	gga Gly	ttt Phe 235	aaa Lys	agg Arg	gct Ala	tat Tyr	gaa Glu 240	720
ttg Leu	gtt Val	aga Arg	agt Ser	ggt Gly 245	gta Val	gct Ala	aag Lys	gat Asp	gtt Val 250	ttg Leu	aaa Lys	aaa Lys	gag Glu	gtt Val 255	gaa Glu	768
tac Tyr	tac Tyr	gat Asp	gag Glu 260	att Ile	aag Lys	agg Arg	ata Ile	ttt Phe 265	aaa Lys	gag Glu	cca Pro	aag Lys	gtt Val 270	acc Thr	gat Asp	816
aac Asn	tat Tyr	tca Ser 275	tta Leu	agc Ser	cta Leu	aaa Lys	ttg Leu 280	cca Pro	gat Asp	aaa Lys	gag Glu	gga Gly 285	att Ile	ata Ile	aaa Lys	864
ttc Phe 290	tta Leu	gtt Val	gat Asp	gaa Glu	aat Asn	gac Asp 295	ttt Phe	aat Asn	tat Tyr	gat Asp	agg Arg 300	gtt Val	aaa Lys	aag Lys	cat His	912

gtt	gat	aaa	ctc	tat	aac	tta	att	gca	aac	aaa	act	aag	caa	aaa	aca	960
Val	Asp	Lys	Leu	Tyr	Asn	Leu	Ile	Ala	Asn	Lys	Thr	Lys	Gln	Lys	Thr	
305					310					315					320	

tta	gat	gca	tgg	ttt	aaa	taa	981
Leu	Asp	Ala	Trp	Phe	Lys		
				325			

<210> 111
 <211> 326
 <212> PRT
 <213> Methanococcus jannaschii

<400> 111																	
Met	Gly	Val	Gln	Phe	Gly	Asp	Phe	Ile	Pro	Lys	Asn	Ile	Ile	Ser	Phe		
1				5					10					15			
Glu	Asp	Leu	Lys	Gly	Lys	Lys	Val	Ala	Ile	Asp	Gly	Met	Asn	Ala	Leu		
			20					25					30				
Tyr	Gln	Phe	Leu	Thr	Ser	Ile	Arg	Leu	Arg	Asp	Gly	Ser	Pro	Leu	Arg		
		35					40					45					
Asn	Arg	Lys	Gly	Glu	Ile	Thr	Ser	Ala	Tyr	Asn	Gly	Val	Phe	Tyr	Lys		
	50					55					60						
Thr	Ile	His	Leu	Leu	Glu	Asn	Asp	Ile	Thr	Pro	Ile	Trp	Val	Phe	Asp		
65					70					75					80		
Gly	Glu	Pro	Pro	Lys	Leu	Lys	Glu	Lys	Thr	Arg	Lys	Val	Arg	Arg	Glu		
				85					90					95			
Met	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Met	Lys	Glu	Ala	Ile	Lys	Lys	Glu		
			100					105					110				
Asp	Phe	Glu	Glu	Ala	Ala	Lys	Tyr	Ala	Lys	Arg	Val	Ser	Tyr	Leu	Thr		
		115					120					125					
Pro	Lys	Met	Val	Glu	Asn	Cys	Lys	Tyr	Leu	Leu	Ser	Leu	Met	Gly	Ile		
	130					135					140						
Pro	Tyr	Val	Glu	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met		
145					150					155					160		
Ala	Lys	Lys	Gly	Asp	Val	Trp	Ala	Val	Val	Ser	Gln	Asp	Tyr	Asp	Ala		
				165					170					175			
Leu	Leu	Tyr	Gly	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Thr	Thr	Lys		
			180					185					190				
Glu	Met	Pro	Glu	Leu	Ile	Glu	Leu	Asn	Glu	Val	Leu	Glu	Asp	Leu	Arg		
		195					200					205					
Ile	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp		
	210					215					220						
Tyr	Asn	Pro	Gly	Gly	Val	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu		
225					230					235					240		
Leu	Val	Arg	Ser	Gly	Val	Ala	Lys	Asp	Val	Leu	Lys	Lys	Glu	Val	Glu		
				245					250					255			

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
 260 265 270
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
 275 280 285
 Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
 290 295 300
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320
 Leu Asp Ala Trp Phe Lys
 325

<210> 112
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 112
 gaggtgatac catgggtgtc c 21

<210> 113
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 113
 gaaactctgc agcgcgtcag 20

<210> 114
 <211> 1023
 <212> DNA
 <213> Pyrococcus furiosus

<220>
 <221> CDS
 <222> (1) .. (1020)

<400> 114
 atg ggt gtc cca att ggt gag att ata cca aga aaa gaa att gag tta 48
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15
 gaa aac cta tac ggg aaa aaa atc gca atc gac gct ctt aat gca atc 96
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 tac caa ttt ttg tcc aca ata aga cag aaa gat gga act cca ctt atg 144
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45

gat	tca	aag	ggt	aga	ata	acc	tcc	cac	cta	agc	ggg	ctc	ttt	tac	agg	192
Asp	Ser	Lys	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Leu	Phe	Tyr	Arg	
	50					55					60					
aca	ata	aac	cta	atg	gag	gct	gga	ata	aaa	cct	gtg	tat	gtt	ttt	gat	240
Thr	Ile	Asn	Leu	Met	Glu	Ala	Gly	Ile	Lys	Pro	Val	Tyr	Val	Phe	Asp	
	65				70					75					80	
gga	gaa	cct	cca	gaa	ttc	aaa	aag	aaa	gag	ctc	gaa	aaa	aga	aga	gaa	288
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Lys	Glu	Leu	Glu	Lys	Arg	Arg	Glu	
				85					90					95		
gcg	aga	gag	gaa	gct	gaa	gaa	aag	tgg	aga	gaa	gca	ctt	gaa	aaa	gga	336
Ala	Arg	Glu	Glu	Ala	Glu	Glu	Lys	Trp	Arg	Glu	Ala	Leu	Glu	Lys	Gly	
			100					105					110			
gag	ata	gag	gaa	gca	aga	aaa	tat	gcc	caa	aga	gca	acc	agg	gta	aat	384
Glu	Ile	Glu	Glu	Ala	Arg	Lys	Tyr	Ala	Gln	Arg	Ala	Thr	Arg	Val	Asn	
		115					120					125				
gaa	atg	ctc	atc	gag	gat	gca	aaa	aaa	ctc	tta	gag	ctt	atg	gga	att	432
Glu	Met	Leu	Ile	Glu	Asp	Ala	Lys	Lys	Leu	Leu	Glu	Leu	Met	Gly	Ile	
	130					135					140					
cct	ata	gtt	caa	gca	cct	agc	gag	gga	gag	gcc	caa	gct	gca	tat	atg	480
Pro	Ile	Val	Gln	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	
	145				150					155					160	
gcc	gca	aag	ggg	agc	gtg	tat	gca	tcg	gct	agt	caa	gat	tac	gat	tcc	528
Ala	Ala	Lys	Gly	Ser	Val	Tyr	Ala	Ser	Ala	Ser	Gln	Asp	Tyr	Asp	Ser	
				165				170						175		
cta	ctt	ttt	gga	gct	cca	aga	ctt	gtt	aga	aac	tta	aca	ata	aca	gga	576
Leu	Leu	Phe	Gly	Ala	Pro	Arg	Leu	Val	Arg	Asn	Leu	Thr	Ile	Thr	Gly	
			180					185					190			
aaa	aga	aag	ttg	cct	ggg	aaa	aat	gtc	tac	gtc	gag	ata	aag	ccc	gag	624
Lys	Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Glu	Ile	Lys	Pro	Glu	
		195				200						205				
ttg	ata	att	ttg	gag	gaa	gta	ctc	aag	gaa	tta	aag	cta	aca	aga	gaa	672
Leu	Ile	Ile	Leu	Glu	Glu	Val	Leu	Lys	Glu	Leu	Lys	Leu	Thr	Arg	Glu	
	210					215					220					
aag	ctc	att	gaa	cta	gca	atc	ctc	gtt	gga	aca	gac	tac	aac	cca	gga	720
Lys	Leu	Ile	Glu	Leu	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Pro	Gly	
	225				230				235						240	
gga	ata	aag	ggc	ata	ggc	ctt	aaa	aaa	gct	tta	gag	att	gtt	aga	cac	768
Gly	Ile	Lys	Gly	Ile	Gly	Leu	Lys	Lys	Ala	Leu	Glu	Ile	Val	Arg	His	
			245					250						255		
tca	aaa	gat	ccg	cta	gca	aag	ttc	caa	aag	caa	agc	gat	gtg	gat	tta	816
Ser	Lys	Asp	Pro	Leu	Ala	Lys	Phe	Gln	Lys	Gln	Ser	Asp	Val	Asp	Leu	
			260					265					270			
tat	gca	ata	aaa	gag	ttc	ttc	cta	aac	cca	cca	gtc	aca	gat	aac	tac	864
Tyr	Ala	Ile	Lys	Glu	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asn	Tyr	
		275					280					285				

aat tta gtg tgg aga gat ccc gac gaa gag gga ata cta aag ttc tta	912
Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu	
290 295 300	
tgt gac gag cat gac ttt agt gag gaa aga gta aag aat gga tta gag	960
Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu	
305 310 315 320	
agg ctt aag aag gca atc aaa agt gga aaa caa tca acc ctt gaa agt	1008
Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser	
325 330 335	
tgg ttc aag aga taa	1023
Trp Phe Lys Arg	
340	

<210> 115
 <211> 340
 <212> PRT
 <213> Pyrococcus furiosus

<400> 115	
Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu	
1 5 10 15	
Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile	
20 25 30	
Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met	
35 40 45	
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg	
50 55 60	
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp	
65 70 75 80	
Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu	
85 90 95	
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly	
100 105 110	
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn	
115 120 125	
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile	
130 135 140	
Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met	
145 150 155 160	
Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser	
165 170 175	
Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly	
180 185 190	
Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu	
195 200 205	

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220
 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335
 Trp Phe Lys Arg
 340

<210> 116
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 116
 gataccatgg gtgtcccaat tgggtg

25

<210> 117
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 117
 tcgacgtcga cttatctctt gaaccaactt tcaaggg

37

<210> 118
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 118
 agcgagggag aggcccaagc

20

<210> 119
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 119
 gcctatgccc tttattcctc c 21

<210> 120
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 120
 tggtcgctgt ctcgctgaaa gcgagacagc gtg 33

<210> 121
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 121
 tgctctctgg tcgctgtctg aaagacagcg 30

<210> 122
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 122
 cgagagacca cgct 14

<210> 123
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 123
 ttttccagag cctaataaaa ttaggctctg gaaagacgct cgtg 44

<210> 124
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 124
 aacgagcgtc tttg 14

<210> 125
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 125
 aacgagcgtc attg 14

<210> 126
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 126
 ttttttttta attaggctct ggaaagacgc tcgtgaaacg agcgtctttg d 51

<210> 127
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 127
 ttttccagag cctaag 17

<210> 128
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 128
 tggctatagr ccagggccac 20

<210> 129
 <211> 2505
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(2499)

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 129
 atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc 192
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg 240
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa 288
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc 336
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag 384
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa 432
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag 480
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg 528
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac 576
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

aac	ctt	ccc	ggg	gtc	aag	ggc	atc	ggg	gag	aag	acg	gcg	agg	aag	ctt	624
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	
		195					200					205				
ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac	cgg	672
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
ctg	aag	ccc	gcc	atc	cgg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat	ctg	720
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	
	225				230					235					240	
aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	cgc	acc	gac	ctg	ccc	ctg	gag	768
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	
				245					250					255		
gtg	gac	ttc	gcc	aaa	agg	cgg	gag	ccc	gac	cgg	gag	agg	ctt	agg	gcc	816
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	
			260					265					270			
ttt	ctg	gag	agg	ctt	gag	ttt	ggc	agc	ctc	ctc	cac	gag	ttc	ggc	ctt	864
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	
		275					280					285				
ctg	gaa	agc	ccc	aag	gcc	ctg	gag	gag	gcc	ccc	tgg	ccc	ccg	ccg	gaa	912
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	
	290					295					300					
ggg	gcc	ttc	gtg	ggc	ttt	gtg	ctt	tcc	cgc	aag	gag	ccc	atg	tgg	gcc	960
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	
	305				310					315					320	
gat	ctt	ctg	gcc	ctg	gcc	gcc	gcc	agg	ggg	ggc	cgg	gtc	cac	cgg	gcc	1008
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	
				325					330					335		
ccc	gag	cct	tat	aaa	gcc	ctc	agg	gac	ctg	aag	gag	gcg	cgg	ggg	ctt	1056
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	
			340					345					350			
ctc	gcc	aaa	gac	ctg	agc	gtt	ctg	gcc	ctg	agg	gaa	ggc	ctt	ggc	ctc	1104
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	
		355					360					365				
ccg	ccc	ggc	gac	gac	ccc	atg	ctc	ctc	gcc	tac	ctc	ctg	gac	cct	tcc	1152
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
	370					375					380					
aac	acc	acc	ccc	gag	ggg	gtg	gcc	cgg	cgc	tac	ggc	ggg	gag	tgg	acg	1200
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
	385				390					395					400	
gag	gag	gcg	ggg	gag	cgg	gcc	gcc	ctt	tcc	gag	agg	ctc	ttc	gcc	aac	1248
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	
			405					410					415			
ctg	tgg	ggg	agg	ctt	gag	ggg	gag	gag	agg	ctc	ctt	tgg	ctt	tac	cgg	1296
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
			420				425					430				
gag	gtg	gag	agg	ccc	ctt	tcc	gct	gtc	ctg	gcc	cac	atg	gag	gcc	acg	1344
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	

435					440					445						
ggg Gly 450	gtg Val	cgc Arg	ctg Leu	gac Asp	gtg Val	gcc Ala 455	tat Tyr	ctc Leu	agg Arg	gcc Ala 460	ttg Leu	tcc Ser	ctg Leu	gag Glu	gtg Val	1392
gcc Ala 465	ggg Gly	gag Glu	atc Ile	gcc Ala	cgc Arg 470	ctc Leu	gag Glu	gcc Ala	gag Glu	gtc Val 475	ttc Phe	cgc Arg	ctg Leu	gcc Ala	ggc Gly 480	1440
cac His	ccc Pro	ttc Phe	aac Asn 485	ctc Leu	aac Asn	tcc Ser	cgg Arg	gac Asp 490	cag Gln	ctg Leu	gaa Glu	agg Arg	gtc Val 495	ctc Leu	ttt Phe	1488
gac Asp	gag Glu	cta Leu	ggg Gly 500	ctt Leu	ccc Pro	gcc Ala	atc Ile	ggc Gly 505	aag Lys	acg Thr	gag Glu	aag Lys	acc Thr 510	ggc Gly	aag Lys	1536
cgc Arg	tcc Ser 515	acc Thr	agc Ser	gcc Ala	gcc Ala	gtc Val 520	ctg Leu	gag Glu	gcc Ala	ctc Leu	cgc Arg 525	gag Glu	gcc Ala	cac His	ccc Pro	1584
atc Ile 530	gtg Val	gag Glu	aag Lys	atc Ile	ctg Leu	cag Gln 535	tac Tyr	cgg Arg	gag Glu	ctc Leu	acc Thr 540	aag Lys	ctg Leu	aag Lys	agc Ser	1632
acc Thr 545	tac Tyr	att Ile	gac Asp	ccc Pro	ttg Leu 550	ccg Pro	gac Asp	ctc Leu	atc Ile	cac His 555	ccc Pro	agg Arg	acg Thr	ggc Gly	cgc Arg 560	1680
ctc Leu	cac His	acc Thr	cgc Arg 565	ttc Phe	aac Asn	cag Gln	acg Thr	gcc Ala 570	acg Thr	gcc Ala	acg Thr	ggc Gly	agg Arg	cta Leu 575	agt Ser	1728
agc Ser	tcc Ser	gat Asp 580	ccc Pro	aac Asn	ctc Leu	cag Gln	aac Asn	atc Ile 585	ccc Pro	gtc Val	cgc Arg	acc Thr 590	ccg Pro	ctt Leu	ggg Gly	1776
cag Gln 595	agg Arg	atc Ile	cgc Arg	cgg Arg	gcc Ala	ttc Phe 600	atc Ile	gcc Ala	gag Glu	gag Glu	ggg Gly 605	tgg Trp	cta Leu	ttg Leu	gtg Val	1824
gcc Ala 610	ctg Leu	gcc Ala	tat Tyr	agc Ser	cag Gln	ata Ile 615	gag Glu	ctc Leu	agg Arg	gtg Val 620	ctg Leu	gcc Ala	cac His	ctc Leu	tcc Ser	1872
ggc Gly 625	gac Asp	gag Glu	aac Asn	ctg Leu	atc Ile 630	cgg Arg	gtc Val	ttc Phe	cag Gln	gag Glu 635	ggg Gly	cgg Arg	gac Asp	atc Ile	cac His 640	1920
acg Thr	gag Glu	acc Thr	gcc Ala 645	agc Ser	tgg Trp	atg Met	ttc Phe	ggc Gly 650	gtc Val	ccc Pro	cgg Arg	gag Glu	gcc Ala 655	gtg Val	gac Asp	1968
ccc Pro	ctg Leu	atg Met	cgc Arg 660	cgg Arg	gcg Ala	gcc Ala	aag Lys 665	acc Thr	atc Ile	aac Asn	ttc Phe	ggg Gly 670	gtc Val	ctc Leu	tac Tyr	2016
ggc Gly 675	atg Met	tcg Ser	gcc Ala	cac His	cgc Arg	ctc Leu 680	tcc Ser	cag Gln	gag Glu	cta Leu	gcc Ala 685	atc Ile	cct Pro	tac Tyr	gag Glu	2064

gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg	2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val	
690 695 700	
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac	2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr	
705 710 715 720	
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc	2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala	
725 730 735	
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
820 825 830	
gag tgatag	2505
Glu	

<210> 130
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 130
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val 65	Val	Phe	Asp	Ala	Lys 70	Ala	Pro	Ser	Phe	Arg 75	His	Glu	Ala	Tyr	Gly 80
Gly	Tyr	Lys	Ala	Gly 85	Arg	Ala	Pro	Thr	Pro 90	Glu	Asp	Phe	Pro	Arg 95	Gln
Leu	Ala	Leu	Ile 100	Lys	Glu	Leu	Val	Asp 105	Leu	Leu	Gly	Leu	Ala	Arg	Leu
Glu	Val	Pro 115	Gly	Tyr	Glu	Ala	Asp 120	Asp	Val	Leu	Ala	Ser 125	Leu	Ala	Lys
Lys 130	Ala	Glu	Lys	Glu	Gly	Tyr 135	Glu	Val	Arg	Ile	Leu 140	Thr	Ala	Asp	Lys
Asp 145	Leu	Tyr	Gln	Leu	Leu 150	Ser	Asp	Arg	Ile	His 155	Val	Leu	His	Pro	Glu 160
Gly	Tyr	Leu	Ile	Thr 165	Pro	Ala	Trp	Leu	Trp 170	Glu	Lys	Tyr	Gly	Leu 175	Arg
Pro	Asp	Gln	Trp 180	Ala	Asp	Tyr	Arg	Ala 185	Leu	Thr	Gly	Asp	Glu	Ser	Asp
Asn	Leu	Pro 195	Gly	Val	Lys	Gly	Ile 200	Gly	Glu	Lys	Thr	Ala 205	Arg	Lys	Leu
Leu	Glu 210	Glu	Trp	Gly	Ser	Leu	Glu 215	Ala	Leu	Leu	Lys 220	Asn	Leu	Asp	Arg
Leu 225	Lys	Pro	Ala	Ile	Arg 230	Glu	Lys	Ile	Leu	Ala 235	His	Met	Asp	Asp	Leu 240
Lys	Leu	Ser	Trp	Asp 245	Leu	Ala	Lys	Val	Arg 250	Thr	Asp	Leu	Pro	Leu 255	Glu
Val	Asp	Phe	Ala 260	Lys	Arg	Arg	Glu	Pro 265	Asp	Arg	Glu	Arg	Leu	Arg	Ala
Phe	Leu	Glu 275	Arg	Leu	Glu	Phe	Gly 280	Ser	Leu	Leu	His	Glu 285	Phe	Gly	Leu
Leu	Glu 290	Ser	Pro	Lys	Ala	Leu	Glu 295	Glu	Ala	Pro	Trp 300	Pro	Pro	Pro	Glu
Gly 305	Ala	Phe	Val	Gly	Phe 310	Val	Leu	Ser	Arg	Lys 315	Glu	Pro	Met	Trp	Ala 320
Asp	Leu	Leu	Ala	Leu 325	Ala	Ala	Ala	Arg	Gly 330	Gly	Arg	Val	His	Arg 335	Ala
Pro	Glu	Pro	Tyr 340	Lys	Ala	Leu	Arg	Asp 345	Leu	Lys	Glu	Ala	Arg	Gly	Leu
Leu	Ala	Lys 355	Asp	Leu	Ser	Val	Leu 360	Ala	Leu	Arg	Glu	Gly 365	Leu	Gly	Leu
Pro 370	Pro	Gly	Asp	Asp	Pro	Met 375	Leu	Leu	Ala	Tyr	Leu 380	Leu	Asp	Pro	Ser
Asn 385	Thr	Thr	Pro	Glu	Gly 390	Val	Ala	Arg	Arg	Tyr 395	Gly	Gly	Glu	Trp	Thr 400

Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	405	410	415
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	420	425	430
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	500	505	510
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	530	535	540
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605
Ala	Leu	Ala	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	725	730	735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu

<210> 131
 <211> 2505
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(2499)

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 131
 atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc 192
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg 240
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa 288
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc 336
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110

gag	gtc	ccg	ggc	tac	gag	gcg	gac	gac	gtc	ctg	gcc	agc	ctg	gcc	aag	384
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	
		115					120					125				
aag	gcg	gaa	aag	gag	ggc	tac	gag	gtc	cgc	atc	ctc	acc	gcc	gac	aaa	432
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	
	130					135					140					
gac	ctt	tac	cag	ctc	ctt	tcc	gac	cgc	atc	cac	gtc	ctc	cac	ccc	gag	480
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	
145					150					155					160	
ggg	tac	ctc	atc	acc	ccg	gcc	tgg	ctt	tgg	gaa	aag	tac	ggc	ctg	agg	528
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	
				165					170					175		
ccc	gac	cag	tgg	gcc	gac	tac	cgg	gcc	ctg	acc	ggg	gac	gag	tcc	gac	576
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
			180					185					190			
aac	ctt	ccc	ggg	gtc	aag	ggc	atc	ggg	gag	aag	acg	gcg	agg	aag	ctt	624
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	
		195					200					205				
ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac	cgg	672
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
ctg	aag	ccc	gcc	atc	cgg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat	ctg	720
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	
225					230					235					240	
aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	cgc	acc	gac	ctg	ccc	ctg	gag	768
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	
				245					250					255		
gtg	gac	ttc	gcc	aaa	agg	cgg	gag	ccc	gac	cgg	gag	agg	ctt	agg	gcc	816
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	
			260					265					270			
ttt	ctg	gag	agg	ctt	gag	ttt	ggc	agc	ctc	ctc	cac	gag	ttc	ggc	ctt	864
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	
		275					280					285				
ctg	gaa	agc	ccc	aag	gcc	ctg	gag	gag	gcc	ccc	tgg	ccc	ccg	ccg	gaa	912
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	
	290					295					300					
ggg	gcc	ttc	gtg	ggc	ttt	gtg	ctt	tcc	cgc	aag	gag	ccc	atg	tgg	gcc	960
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	
305					310					315					320	
gat	ctt	ctg	gcc	ctg	gcc	gcc	gcc	agg	ggg	ggc	cgg	gtc	cac	cgg	gcc	1008
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	
				325					330					335		
ccc	gag	cct	tat	aaa	gcc	ctc	agg	gac	ctg	aag	gag	gcg	cgg	ggg	ctt	1056
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	
			340					345					350			

ctc	gcc	aaa	gac	ctg	agc	gtt	ctg	gcc	ctg	agg	gaa	ggc	ctt	ggc	ctc	1104
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	
		355					360					365				
ccg	ccc	ggc	gac	gac	ccc	atg	ctc	ctc	gcc	tac	ctc	ctg	gac	cct	tcc	1152
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
	370					375					380					
aac	acc	acc	ccc	gag	ggg	gtg	gcc	cgg	cgc	tac	ggc	ggg	gag	tgg	acg	1200
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
385					390					395					400	
gag	gag	gcg	ggg	gag	cgg	gcc	gcc	ctt	tcc	gag	agg	ctc	ttc	gcc	aac	1248
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	
				405					410					415		
ctg	tgg	ggg	agg	ctt	gag	ggg	gag	gag	agg	ctc	ctt	tgg	ctt	tac	cgg	1296
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
			420				425						430			
gag	gtg	gag	agg	ccc	ctt	tcc	gct	gtc	ctg	gcc	cac	atg	gag	gcc	acg	1344
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				
ggg	gtg	cgc	ctg	gac	gtg	gcc	tat	ctc	agg	gcc	ttg	tcc	ctg	gag	gtg	1392
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	
	450					455					460					
gcc	ggg	gag	atc	gcc	cgc	ctc	gag	gcc	gag	gtc	ttc	cgc	ctg	gcc	ggc	1440
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
465					470					475					480	
cac	ccc	ttc	aac	ctc	aac	tcc	cgg	gac	cag	ctg	gaa	agg	gtc	ctc	ttt	1488
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
				485					490					495		
gac	gag	cta	ggg	ctt	ccc	gcc	atc	ggc	aag	acg	gag	aag	acc	ggc	aag	1536
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	
			500					505					510			
cgc	tcc	acc	agc	gcc	gcc	gtc	ctg	gag	gcc	ctc	cgc	gag	gcc	cac	ccc	1584
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
		515					520					525				
atc	gtg	gag	aag	atc	ctg	cag	tac	cgg	gag	ctc	acc	aag	ctg	aag	agc	1632
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
	530					535					540					
acc	tac	att	gac	ccc	ttg	ccg	gac	ctc	atc	cac	ccc	agg	acg	ggc	cgc	1680
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
545					550					555					560	
ctc	cac	acc	cgc	ttc	aac	cag	acg	gcc	acg	gcc	acg	ggc	agg	cta	agt	1728
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565				570						575		
agc	tcc	gat	ccc	aac	ctc	cag	aac	atc	ccc	gtc	cgc	acc	ccg	ctt	ggg	1776
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			

cag	agg	atc	cgc	cgg	gcc	ttc	atc	gcc	gag	gag	ggg	tgg	cta	ttg	gtg	1824
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
		595					600					605				
gcc	ctg	gtc	tat	agc	cag	ata	gag	ctc	agg	gtg	ctg	gcc	cac	ctc	tcc	1872
Ala	Leu	Val	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
		610					615				620					
ggc	gac	gag	aac	ctg	atc	cgg	gtc	ttc	cag	gag	ggg	cgg	gac	atc	cac	1920
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
		625					630				635				640	
acg	gag	acc	gcc	agc	tgg	atg	ttc	ggc	gtc	ccc	cgg	gag	gcc	gtg	gac	1968
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	
					645				650					655		
ccc	ctg	atg	cgc	cgg	gcg	gcc	aag	acc	atc	aac	ttc	ggg	gtc	ctc	tac	2016
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
					660				665					670		
ggc	atg	tcg	gcc	cac	cgc	ctc	tcc	cag	gag	cta	gcc	atc	cct	tac	gag	2064
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
							680									
gag	gcc	cag	gcc	ttc	att	gag	cgc	tac	ttt	cag	agc	ttc	ccc	aag	gtg	2112
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	
							695					700				
cgg	gcc	tgg	att	gag	aag	acc	ctg	gag	gag	ggc	agg	agg	cgg	ggg	tac	2160
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	
							710				715				720	
gtg	gag	acc	ctc	ttc	ggc	cgc	cgc	cgc	tac	gtg	cca	gac	cta	gag	gcc	2208
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	
							725							735		
cgg	gtg	aag	agc	gtg	cgg	gag	gcg	gcc	gag	cgc	atg	gcc	ttc	aac	atg	2256
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	
									745					750		
ccc	gtc	cag	ggc	acc	gcc	gcc	gac	ctc	atg	aag	ctg	gct	atg	gtg	aag	2304
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	
							760							765		
ctc	ttc	ccc	agg	ctg	gag	gaa	atg	ggg	gcc	agg	atg	ctc	ctt	cag	gtc	2352
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	
							775					780				
cac	gac	gag	ctg	gtc	ctc	gag	gcc	cca	aaa	gag	agg	gcg	gag	gcc	gtg	2400
His	Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	
							790				795				800	
gcc	cgg	ctg	gcc	aag	gag	gtc	atg	gag	ggg	gtg	tat	ccc	ctg	gcc	gtg	2448
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	
							805				810				815	
ccc	ctg	gag	gtg	gag	gtg	ggg	ata	ggg	gag	gac	tgg	ctc	tcc	gcc	aag	2496
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	
									825					830		
gag	tgatag															2505
Glu																

<210> 132
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 132

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145				150					155						160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225				230						235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		

Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
				325					330					335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
			340					345					350		
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
		355					360					365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
	370					375					380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
385					390					395					400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
				405					410					415	
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg
			420					425					430		
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr
		435					440					445			
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
	450					455					460				
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485						490					495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys
			500					505					510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515					520					525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser
	530					535					540				
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg
545					550					555					560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
				565					570					575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
			580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val
		595					600					605			

Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu

<210> 133

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 133

aaaattcctt tctctttgcc ctttgcttcc

30

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<210> 134
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(2)
<223> The residues at these positions are a
      2'deoxycytosine 5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (4)..(5)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (6)..(8)
<223> The residues at these positions are a
      2'deoxythymidine 5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxyguanosine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (10)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate) .

<220>
<223> Description of Artificial Sequence:  Synthetic

<400> 134
cctaatttgc cagttacaaa ataaacagcc c
31

<210> 135
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic

<400> 135
tgtggaattg tgagcgg
17

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<210> 136
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 136
tggaggctct ccatcaaaaa c 21

<210> 137
<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 137
tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatggga gtgcagtttg 60
gtgattttat tccaaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120
ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatggttctc 180
cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
tacatttggt agagaatgat ataactccaa tctggggttt tgatggagag cctcca 296

<210> 138
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 138
taatctgtat caggctg 17

<210> 139
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 139
gtttttgatg gagagcctcc a 21

<210> 140
<211> 889
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 140

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gtttttgatg gagagcctcc agaattcaaa aagaaagagc tcgaaaaaag aagagaagcg 60
agagaggaag ctgaagaaaa gtggagagaa gcacttgaaa aaggagagat agaggaagca 120
agaaaatatg cccaaagagc aaccagggtta aatgaaatgc tcatcgagga tgcaaaaaaa 180
ctcttagagc ttatgggaat tcctatagtt caagcaccta gcgagggaga ggcccaagct 240
gcatatatgg ccgcaaaggg gagcgtgtat gcatcggcta gtcaagatta cgattcccta 300
ctttttggag ctccaagact tgttagaaac ttaacaataa caggaaaaag aaagttgcct 360
gggaaaaatg tctacgtcga gataaagccc gagttgataa ttttggagga agtactcaag 420
gaattaaagc taacaagaga aaagctcatt gaactagcaa tcctcgttgg aacagactac 480
aaccaggag gaataaaggg cataggcctt aaaaaagctt tagagattgt tagacactca 540
aaagatccgc tagcaaagtt ccaaagcaa agcgatgtgg atttatatgc aataaaagag 600
ttcttcctaa acccaccagt cacagataac tacaatttag tgtggagaga tcccgacgaa 660
gaggaatac taaagttctt atgtgacgag catgacttta gtgaggaaag agtaaagaat 720
ggattagaga ggcttaagaa ggcaatcaaa agtggaaaac aatcaaccct tgaaagttgg 780
ttcaagagat aaccttaaag tctattgcaa tgttatactg acgcgctgca ggcatgcaag 840
cttggctggt ttggcggatg agagaagatt ttcagcctga tacagatta 889
```

<210> 141
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 141

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tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatggga gtgcagtttg 60
gtgattttat tccaaaaaat attatctcct ttgaagattt aaaagggaag aaagtagcta 120
ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatggttctc 180
cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
tacatttggt agagaatgat ataactccaa tctgggtttt tgatggagag cctccagaat 300
tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360
gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccaa agagcaacca 420
```

```

gggtaaatga aatgctcatc gaggatgcaa aaaaactctt agagcttatg ggaattccta 480
tagttcaagc acctagcgag ggagaggccc aagctgcata tatggccgca aaggggagcg 540
tgtatgcacg ggctagtcaa gattacgatt ccctactttt tggagctcca agacttgtaa 600
gaaacttaac aataacagga aaaagaaagt tgccctgggaa aaatgtctac gtcgagataa 660
agccccgagtt gataattttg gaggaagtac tcaaggaatt aaagctaaca agagaaaagc 720
tcattgaact agcaatcctc gttggaacag actacaaccc aggaggaata aagggcatag 780
gccttaaaaa agcttttagag attgttagac actcaaaaga tccgctagca aagttccaaa 840
agcaaagcga tgtggattta tatgcaataa aagagttctt cctaaaccca ccagtcacag 900
ataactacaa tttagtgtgg agagatcccc acgaagaggg aataactaaag ttcttatgtg 960
acgagcatga ctttagtgag gaaagagtaa agaattggatt agagaggctt aagaaggcaa 1020
tcaaaagtgg aaaacaatca acccttgaaa gttggttcaa gagataacct taaagtctat 1080
tgcaatgtta tactgacgcg ctgcaggcat gcaagcttgg ctgttttggc ggatgagaga 1140
agattttcag cctgatacag atta 1164

```

<210> 142

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 142

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tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
cacttatgga ttcaaagggt agaataacct cccacctaaag cgggctcttt tacaggacaa 240
taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagag cctcca 296

```

<210> 143

<211> 840

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 143

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gtttttgatg gagagcctcc aaagttaaag gagaaaacaa ggaaagttag gagagagatg 60
aaagagaaag ctgaacttaa gatgaaagag gcaattaaaa aggaggattt tgaagaagct 120
gctaagtatg caaagagggt tagctatcta actccgaaaa tggttgaaaa ctgcaaata 180

```

ttgttaagtt tgatgggcat tccgtatggt gaagctccct ctgagggaga ggcacaagca 240
 agctatatgg caaagaaggg agatgtttgg gcagttgtaa gtcaagatta tgatgccttg 300
 ttatatggag ctccgagagt tgttagaaat ttaacaacta caaaggagat gccagaactt 360
 attgaattaa atgaggtttt agaggattta agaatttctt tggatgattt gatagatata 420
 gccatattta tgggaactga ctataatcca ggaggagtta aaggaatagg atttaaaagg 480
 gcttatgaat tggttagaag tgggtgtagct aaggatgttt tgaaaaaaga gggtgaatac 540
 tacgatgaga ttaagaggat atttaagag ccaaaggtta ccgataacta ttcattaagc 600
 ctaaaattgc cagataaaga ggggaattata aaattcttag ttgatgaaaa tgactttaat 660
 tatgataggg ttaaaaagca tgttgataaa ctctataact taattgcaaa caaaactaag 720
 caaaaaacat tagatgcatg gtttaaataa tttatataat tttgtgggat gtcgacctgc 780
 aggcattgcaa gcttggctgt tttggcggat gagagaagat tttcagcctg atacagatta 840

<210> 144

<211> 1115

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 144

tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggg agaataacct cccacctaag cgggctcttt tacaggacaa 240
 taaacctaata ggaggctgga ataaaacctg tgtatgtttt tgatggagag cctccaaagt 300
 taaaggagaa aacaaggaaa gttaggagag agatgaaaga gaaagctgaa cttaatgaga 360
 aagaggcaat taaaaaggag gattttgaag aagctgctaa gtatgcaaag agggttagct 420
 atctaactcc gaaaatgggt gaaaactgca aatatttggt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggcac aagcaagcta tatggcaaag aaggagatg 540
 tttgggcagt tgtaagtcaa gattatgatg ccttggtata tggagctccg agagttgtta 600
 gaaatttaac aactacaaag gagatgccag aacttattga attaatgag gtttttagagg 660
 atttaagaat ttctttggat gatttgatag atatagccat atttatggga actgactata 720
 atccaggagg agttaagga ataggattta aaagggtta tgaattgggt agaagtgggtg 780
 tagctaagga tgttttgaaa aaagagggtg aatactacga tgagattaag aggatattta 840
 aagagccaaa ggttaccgat aactattcat taagcctaaa attgccagat aaagagggaa 900

ttataaaatt cttagttgat gaaaatgact ttaattatga tagggttaaa aagcatgttg 960
 ataaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacattagat gcatggttta 1020
 aataatttat ataattttgt gggatgtcga cctgcaggca tgcaagcttg gctgttttgg 1080
 cggatgagag aagattttca gcctgataca gatta 1115

<210> 145
 <211> 386
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 145
 tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggt agaataacct cccacctaag cgggctcttt tacaggacaa 240
 taaacctaata ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360
 gagaagcact tgaaaaagga gagata 386

<210> 146
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 146
 tacttagcag cttcttctat ctctcctttt tca 33

<210> 147
 <211> 668
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 147
 gaagaagctg ctaagtatgc aaagagggtt agctatctaa ctccgaaaat gggtgaaaac 60
 tgcaaatatt tgttaagttt gatgggcatt ccgtatgttg aagctccctc tgagggagag 120
 gcacaagcaa gctatatggc aaagaaggga gatgtttggg cagttgtaag tcaagattat 180
 gatgccttgt tatatggagc tccgagagtt gtagaaatt taacaactac aaaggagatg 240

ccagaactta ttgaattaaa tgaggtttta gaggatttaa gaatttcttt ggatgatttg 300
 atagatatag ccatatttat gggaactgac tataatccag gaggagttaa aggaatagga 360
 tttaaaaggg cttatgaatt ggttagaagt ggtgtagcta aggatgtttt gaaaaaagag 420
 gttgaatact acgatgagat taagaggata tttaaagagc caaagggttac cgataactat 480
 tcattaagcc taaaattgcc agataaagag ggaattataa aattcttagt tgatgaaaat 540
 gactttaatt atgatagggg taaaaagcat gttgataaac tctataactt aattgcaaac 600
 aaaactaagc aaaaaacatt agatgcatgg tttaaacacc accaccacca ccactaactg 660
 cagcggta 668

<210> 148
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 148
 taccgctgca gttagtgggtg gtgggtgggtg tgtttaaacc atgcatctaa tgt 53

<210> 149
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 149
 gaagaagctg ctaagta 17

<210> 150
 <211> 1054
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 150
 tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggt agaataacct cccacctaag cgggctcttt tacaggacaa 240
 taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360

gagaagcact tgaaaaagga gagatagaag aagctgctaa gtatgcaaag agggttagct 420
 atctaactcc gaaaatgggtt gaaaactgca aatatttggtt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggcac aagcaagcta tatggcaaag aaggagatg 540
 tttgggcagt tgtaagtcaa gattatgatg ccttggtata tggagctccg agagttgtta 600
 gaaatttaac aactacaaag gagatgccag aacttattga attaaatgag gtttttagagg 660
 atttaagaat ttctttggat gatttgatag atatagccat atttatggga actgactata 720
 atccaggagg agttaaagga ataggattta aaagggctta tgaattgggtt agaagtgggtg 780
 tagctaagga tgttttgaaa aaagagggttg aatactacga tgagattaag aggatattta 840
 aagagccaaa ggttaccgat aactattcat taagcctaaa attgccagat aaagagggaa 900
 ttataaaaatt cttagttgat gaaaatgact ttaattatga taggggttaa aagcatgttg 960
 ataaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacattagat gcatggttta 1020
 aacaccacca ccaccaccac taactgcagc ggta 1054

<210> 151
 <211> 514
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 151
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 ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatgggttctc 180
 cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
 tacatttggt agagaatgat ataactccaa tctgggtttt tgatgggtgag ccaccaaagt 300
 taaaggagaa aacaaggaaa gttaggagag agatgaaaga gaaagctgaa ctttaagatga 360
 aagaggcaat taaaaaggag gatthttgaag aagctgctaa gtatgcaaag agggttagct 420
 atctaactcc gaaaatgggtt gaaaactgca aatatttggtt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggccc aagc 514

<210> 152
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 152
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17

<210> 153
<211> 667
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 153
gagggagagg cccaagctgc atatatggcc gcaaagggga gcgtgtatgc atcggctagt 60
caagattacg attccctact ttttggagct ccaagacttg ttagaaactt aacaataaca 120
ggaaaaagaa agttgcctgg gaaaaatgtc tacgtcgaga taaagcccga gttgataatt 180
ttggaggaag tactcaagga attaaagcta acaagagaaa agctcattga actagcaatc 240
ctcgttggaa cagactacaa ccaggagga ataaagggca taggccttaa aaaagcttta 300
gagattgtta gacactcaaa agatccgcta gcaaagttcc aaaagcaaag cgatgtggat 360
ttatatgcaa taaaagagtt cttcctaaac ccaccagtca cagataacta caatttagtg 420
tgagagatc ccgacgaaga gggaatacta aagttcttat gtgacgagca tgactttagt 480
gaggaaagag taaagaatgg attagagagg cttaagaagg caatcaaaag tggaaaacaa 540
tcaacccttg aaagttgggt caagagataa ccttaaagtc tattgcaatg ttatactgac 600
gcgctgcagg catgcaagct tggctgtttt ggcggatgag agaagatttt cagcctgata 660
cagatta 667

<210> 154
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 154
gagggagagg cccaagc

17

<210> 155
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 155
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 gtgattttat tccaaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120
 ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatggttctc 180
 cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
 tacatttggt agagaatgat ataactccaa tctgggtttt tgatggtgag ccaccaaagt 300
 taaaggagaa aacaaggaaa gttaggagag agatgaaaga gaaagctgaa cttaagatga 360
 aagaggcaat taaaaaggag gattttgaag aagctgctaa gtatgcaaag agggtttagct 420
 atctaactcc gaaaatgggt gaaaactgca aatatttggt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggccc aagctgcata tatggccgca aaggggagcg 540
 tgtatgcacg ggctagtcaa gattacgatt ccctactttt tggagctcca agacttgтта 600
 gaaacttaac aataacagga aaaagaaagt tgcctgggaa aaatgtctac gtcgagataa 660
 agcccgagtt gataattttg gaggaagtac tcaaggaatt aaagctaaca agagaaaagc 720
 tcattgaact agcaatcctc gttggaacag actacaaccc aggaggaata aagggcatag 780
 gccttaaaaa agcttttagag attgtttagac actcaaaaga tccgctagca aagttccaaa 840
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 acgagcatga ctttagtgag gaaagagtaa agaattggatt agagaggctt aagaaggcaa 1020
 tcaaaagtgg aaaacaatca acccttgaaa gttgggtcaa gagataacct taaagtctat 1080
 tgcaatgtta tactgacgcg ctgcaggcat gcaagcttgg ctgttttggc ggatgagaga 1140
 agattttcag cctgatacag atta 1164

<210> 156
 <211> 514
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 156
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 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggt agaataacct cccacctaaag cgggctcttt tacaggacaa 240
 taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360

gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccaa agagcaacca 420
 gggtaaataa aatgctcatc gaggatgcaa aaaaactctt agagcttatg ggaattccta 480
 tagttcaagc acctagcgag ggagaggccc aagc 514

<210> 157
 <211> 618
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 157
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 caagattatg atgccttggt atatggagct ccgagagttg ttagaaattt aacaactaca 120
 aaggagatgc cagaacttat tgaattaaat gaggttttag aggatttaag aatttctttg 180
 gatgatttga tagatatagc catatttatg ggaactgact ataatccagg aggagttaaa 240
 ggaataggat ttaaaagggc ttatgaattg gttagaagtg gtgtagctaa ggatgttttg 300
 aaaaaagagg ttgaatacta cgatgagatt aagaggatat ttaaagagcc aaagggtacc 360
 gataactatt cattaagcct aaaattgcca gataaagagg gaattataaa attcttagtt 420
 gatgaaaatg actttaatta tgatagggtt aaaaagcatg ttgataaact ctataactta 480
 attgcaaaca aaactaagca aaaaacatta gatgcatggt ttaaataatt tatataattt 540
 tgtgggatgt cgacctgcag gcatgcaagc ttggctgttt tggcggatga gagaagattt 600
 tcagcctgat acagatta 618

<210> 158
 <211> 1115
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 158
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 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggt agaataacct cccacctagc cgggctcttt tacaggacaa 240
 taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360
 gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccaa agagcaacca 420

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atccaggagg agttaagga ataggattta aaagggctta tgaattggtt agaagtgggtg 780
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aataatttat ataattttgt gggatgtcga cctgcaggca tgcaagcttg gctgttttgg 1080
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<210> 159

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 159

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aaggccgtct tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240
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gcccaggggc gggagcccga ccgggagggg cttagggcct tcctggagag gctggagttc 840

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<210> 160
 <211> 834
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 160

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Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
			35				40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
	65				70					75					80
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
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	210					215					220				
Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	Glu	Asp
	225				230					235					240
Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu
			245						250					255	
Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			

Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	
290						295					300					
Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	
305					310					315					320	
Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val	His	Arg	
				325					330					335		
Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	
			340					345					350			
Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	
		355					360					365				
Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	
	370					375					380					
Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	
385					390					395					400	
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	
				405					410					415		
Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	
			420					425					430			
His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	
		435					440					445				
Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	
	450					455					460					
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	
465					470					475					480	
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	
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Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly	
			500					505					510			
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	
		515					520					525				
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	
	530					535					540					
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	
545					550					555					560	
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	
				565					570					575		
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	
			580					585					590			
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	
		595					600					605				
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	
	610					615					620					

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830

Lys Gly

<210> 161

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 161

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caggcccttt ccctggagct tgcggaggag atccgcccgc tcgaggagga ggtcttccgc 1440
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gagcttaggc ttcccgctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg 1680
acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgaccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgcccg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgctcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgaggc cgtggacccc 1980
ctgatgcgcc gggcgccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catcccctac gaggagcgcg tggcctttat agagcgctac 2100
ttccaaagct tcccaagggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcacct caacgcccgg 2220
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 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcacgc tcctccaggt ccacgacgag ctctctctgg aggcccccca agcgcggggc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtta g 2511

<210> 162

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 162

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	

Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
210						215				220					
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315					320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val
			340					345					350		
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly
		355					360					365			
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu
	370					375					380				
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly
385					390					395					400
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu
				405					410					415	
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp
			420					425					430		
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met
		435					440					445			
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser
	450					455					460				
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg
465					470					475					480
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg
				485				490						495	
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys
			500					505					510		
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu
		515					520					525			
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys
	530					535					540				

Leu 545	Lys	Asn	Thr	Tyr	Val 550	Asp	Pro	Leu	Pro	Ser 555	Leu	Val	His	Pro	Arg 560
Thr	Gly	Arg	Leu	His 565	Thr	Arg	Phe	Asn	Gln 570	Thr	Ala	Thr	Ala	Thr	Gly 575
Arg	Leu	Ser	Ser 580	Ser	Asp	Pro	Asn	Leu 585	Gln	Asn	Ile	Pro	Val	Arg	Thr
Pro	Leu	Gly 595	Gln	Arg	Ile	Arg	Arg 600	Ala	Phe	Val	Ala	Glu 605	Ala	Gly	Trp
Ala 610	Leu	Val	Ala	Leu	Asp	Tyr 615	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
His 625	Leu	Ser	Gly	Asp	Glu 630	Asn	Leu	Ile	Arg	Val 635	Phe	Gln	Glu	Gly	Lys 640
Asp	Ile	His	Thr	Gln 645	Thr	Ala	Ser	Trp	Met 650	Phe	Gly	Val	Pro	Pro	Glu 655
Ala	Val	Asp	Pro 660	Leu	Met	Arg	Arg	Ala 665	Ala	Lys	Thr	Val	Asn	Phe	Gly 670
Val	Leu	Tyr 675	Gly	Met	Ser	Ala	His 680	Arg	Leu	Ser	Gln	Glu 685	Leu	Ala	Ile
Pro 690	Tyr	Glu	Glu	Ala	Val	Ala 695	Phe	Ile	Glu	Arg	Tyr 700	Phe	Gln	Ser	Phe
Pro 705	Lys	Val	Arg	Ala	Trp 710	Ile	Glu	Lys	Thr	Leu 715	Glu	Glu	Gly	Arg	Lys 720
Arg	Gly	Tyr	Val	Glu 725	Thr	Leu	Phe	Gly	Arg 730	Arg	Arg	Tyr	Val	Pro	Asp 735
Leu	Asn	Ala	Arg 740	Val	Lys	Ser	Val	Arg 745	Glu	Ala	Ala	Glu	Arg 750	Met	Ala
Phe	Asn	Met 755	Pro	Val	Gln	Gly	Thr 760	Ala	Ala	Asp	Leu	Met 765	Lys	Leu	Ala
Met 770	Val	Lys	Leu	Phe	Pro	Arg 775	Leu	Arg	Glu	Met	Gly 780	Ala	Arg	Met	Leu
Leu 785	Gln	Val	His	Asp	Glu 790	Leu	Leu	Leu	Glu	Ala 795	Pro	Gln	Ala	Arg	Ala 800
Glu	Glu	Val	Ala	Ala 805	Leu	Ala	Lys	Glu	Ala 810	Met	Glu	Lys	Ala	Tyr 815	Pro
Leu	Ala	Val	Pro 820	Leu	Glu	Val	Glu	Val 825	Gly	Met	Gly	Glu	Asp 830	Trp	Leu
Ser	Ala	Lys 835	Gly												

<210> 163
<211> 2511
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 163

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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaaccgcc tcgagggtccc cggctacgag 360
gcggaacgac ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag 540
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ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
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gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg 1620
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gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680
 acggggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
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 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
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<210> 164

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 164

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70				75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85					90						95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100					105						110		

Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val	325	330	335
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	340	345	350
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	355	360	365
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	370	375	380
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	405	410	415
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	420	425	430
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	435	440	445

Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser
450						455					460				
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg
465					470					475					480
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg
				485					490					495	
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys
			500					505					510		
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu
		515					520					525			
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys
	530					535					540				
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg
545					550					555					560
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly
				565					570					575	
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr
			580					585					590		
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp
		595					600					605			
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
	610					615					620				
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys
625					630					635					640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
705					710					715					720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
				725					730					735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				

Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 165
 <211> 350
 <212> DNA
 <213> Escherichia coli

<400> 165
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 ggtaacagga agaagcttgc ttctttgctg acgagtggcg gacgggtgag taatgtctgg 120
 gaaactgcct gatggagggg gataactact ggaaacggta gctaataccg cataacgtcg 180
 caagaccaa gagggggacc ttcgggcctc ttgccatcgg atgtgcccag atgggattag 240
 ctagtaggtg gggtaacggc tcacctaggc gacgatccct agctgggtctg agaggatgac 300
 cagccacact ggaactgaga cacggtccag actcctacgg gaggcagcag 350

<210> 166
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 166
 cacgaattcc gaggcgatgc ttccgctc 28

<210> 167
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 167
 tcgacgtcga ctaacccttg gcggaaagcc 30

<210> 168
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 168
 gcatcgctc ggaattcatg gtc 23

<210> 169
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 169
 caggaggagc tcgttgtgga cctgga 26

<210> 170
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 170
 ccgtcaacat ttaccatggg tgcgga 26

<210> 171
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 171
 ccgccacctc gtagtcgaca tccttttcgt g 31

<210> 172
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 172
 gggtgttccc atgggagtta aactcagg 28

<210> 173
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 173
 ctgaattctg cagaaaaagg gg 22

<210> 174
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 174
 agagtttgat cctggctcag 20

<210> 175
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 175
 ctgctgcctc ccgtaggagt 20

<210> 176
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 176
 ttttcgctgt ctcgctgaaa gcgagacagc gttt 34

<210> 177
 <211> 59
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 177
 ttttcgctgt ctcgctgaaa gcgagacagc gaaagacgct cgtgaaacga gcgtctttg 59

<210> 178
 <211> 1011
 <212> DNA
 <213> Archaeoglobus fulgidus

<400> 178
 atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
 ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
 cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180
 atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtggt tgtattcgac 240
 ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggctgag 300
 gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
 caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac 420
 atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
 gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540
 ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgct 600
 tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg 660
 acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg 720
 aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tatttttcagg 780
 gcactcaagg ctctgaaagt aatattgac cacgtagagg agataaggaa tttcttcctg 840
 aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900
 atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag 960
 aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttctg a 1011

<210> 179
 <211> 336
 <212> PRT
 <213> Archaeoglobus fulgidus

<400> 179
 Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
 1 5 10 15
 Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
 20 25 30
 Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80

Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	
				85					90					95		
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	
		100						105					110			
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	
		115					120					125				
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	
	130					135					140					
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	
145					150					155					160	
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	
				165					170					175		
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys	
			180					185					190			
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile	
		195				200						205				
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln	
	210					215					220					
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Glu	Gly	Val	
225					230					235					240	
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly	
				245					250					255		
Asp	Ile	Phe	Arg	Ala	Leu	Lys	Ala	Leu	Lys	Val	Asn	Ile	Asp	His	Val	
			260					265					270			
Glu	Glu	Ile	Arg	Asn	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asp	Tyr	
		275					280					285				
Arg	Ile	Glu	Phe	Arg	Glu	Pro	Asp	Phe	Glu	Lys	Ala	Ile	Glu	Phe	Leu	
	290					295					300					
Cys	Glu	Glu	His	Asp	Phe	Ser	Arg	Glu	Arg	Val	Glu	Lys	Ala	Leu	Glu	
305					310					315					320	
Lys	Leu	Lys	Ala	Leu	Lys	Ser	Thr	Gln	Ala	Thr	Leu	Glu	Arg	Trp	Phe	
				325					330					335		

<210> 180

<211> 777

<212> DNA

<213> Methanobacterium thermoautotrophicum

<400> 180

atgggagtta aactcagga tggtgtatca cccgcagga tacgccttga ggaccttagg 60

ggaagaacgg tcgcagtcga tgcagccaac acactctacc agttcctatc aagcataagg 120

cagagggatg gaacaccct catggattcc aggggtagag taacatcaca cctcagcggc 180

atactctaca ggacggccgc ggtcatggag agggagataa gggatcatata tgtcttcgat 240
 ggaagggtccc accacctcaa gggcgagacc gtgagcagga gggctgatat ccggaagaaa 300
 tctgaggttg agtggaagag ggcccttgag gagggggaca ttgacagggc gaaaaaatat 360
 gctgtaagggt cctcaaggat gtcctcagaa atactggaga gttcaaagag gtccttgga 420
 cttctgggaa taccctatgt acaggcaccg ggtgaggggg aggctcaggc atcatacatg 480
 gttaagatgg gcgatgcatg ggccgtggca tcccaggact atgactgtct cctctttggc 540
 gcccgaaggg ttgtaaggaa cctcaccctc agcggaaaac ttgaggaccc cgagatcatt 600
 gaactggagt ccaccctcag ggaactctca atcagccaca cacagctcgt ggatatggca 660
 ctactcgtcg ggactgactt caatgagggt gtaaagggga taggcgcaag gaggggactc 720
 aaactcatca gggagaaggg cgacattttc aaagtcatca gggaccttga agcttga 777

<210> 181

<211> 258

<212> PRT

<213> Methanobacterium thermoautotrophicum

<400> 181

Met	Gly	Val	Lys	Leu	Arg	Asp	Val	Val	Ser	Pro	Arg	Arg	Ile	Arg	Leu	1	5	10	15
Glu	Asp	Leu	Arg	Gly	Arg	Thr	Val	Ala	Val	Asp	Ala	Ala	Asn	Thr	Leu	20	25	30	
Tyr	Gln	Phe	Leu	Ser	Ser	Ile	Arg	Gln	Arg	Asp	Gly	Thr	Pro	Leu	Met	35	40	45	
Asp	Ser	Arg	Gly	Arg	Val	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg	50	55	60	
Thr	Ala	Ala	Val	Met	Glu	Arg	Glu	Ile	Arg	Val	Ile	Tyr	Val	Phe	Asp	65	70	75	80
Gly	Arg	Ser	His	His	Leu	Lys	Gly	Glu	Thr	Val	Ser	Arg	Arg	Ala	Asp	85	90	95	
Ile	Arg	Lys	Lys	Ser	Glu	Val	Glu	Trp	Lys	Arg	Ala	Leu	Glu	Glu	Gly	100	105	110	
Asp	Ile	Asp	Arg	Ala	Lys	Lys	Tyr	Ala	Val	Arg	Ser	Ser	Arg	Met	Ser	115	120	125	
Ser	Glu	Ile	Leu	Glu	Ser	Ser	Lys	Arg	Leu	Leu	Glu	Leu	Leu	Gly	Ile	130	135	140	
Pro	Tyr	Val	Gln	Ala	Pro	Gly	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met	145	150	155	160
Val	Lys	Met	Gly	Asp	Ala	Trp	Ala	Val	Ala	Ser	Gln	Asp	Tyr	Asp	Cys	165	170	175	
Leu	Leu	Phe	Gly	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Leu	Ser	Gly	180	185	190	

Lys	Leu	Glu	Asp	Pro	Glu	Ile	Ile	Glu	Leu	Glu	Ser	Thr	Leu	Arg	Glu
		195					200					205			
Leu	Ser	Ile	Ser	His	Thr	Gln	Leu	Val	Asp	Met	Ala	Leu	Leu	Val	Gly
	210					215					220				
Thr	Asp	Phe	Asn	Glu	Gly	Val	Lys	Gly	Ile	Gly	Ala	Arg	Arg	Gly	Leu
225					230					235					240
Lys	Leu	Ile	Arg	Glu	Lys	Gly	Asp	Ile	Phe	Lys	Val	Ile	Arg	Asp	Leu
				245					250					255	

Glu Ala

<210> 182
 <211> 987
 <212> DNA
 <213> Methanobacterium thermoautotrophicum

<400> 182
 atgggagtta aactcagga tggtgtatca cccgcagga tacgccttga ggaccttagg 60
 ggaagaacgg tcgcagtcga tgcagccaac acactctacc agttcctatc aagcataagg 120
 cagaggggatg gaacacccct catggattcc aggggtagag taacatcaca cctcagcggc 180
 atactctaca ggacggccgc ggtcatggag agggagataa gggcatata tgtcttcgat 240
 ggaagggtccc accacctcaa gggcgagacc gtgagcagga gggctgatat ccggaagaaa 300
 tctgaggttg agtggaagag ggcccttgag gagggggaca ttgacagggc gagaaaatat 360
 gctgtaaggt cctcaaggat gtcctcagaa atactggaga gttcaaagag gctcctggaa 420
 cttctgggaa taccctatgt acaggcacc ggtgaggggg aggctcaggc atcatacatg 480
 gttaagatgg gcgatgcatg ggccgtggca tcccaggact atgactgtct cctctttggc 540
 gcccgaaggg ttgtaaggaa ggtcaccctc agcggaagaa ttgaggacct ccacatcatt 600
 gaactggagt ccaccctcag ggccctctca atcagccaca cacagctcgt ggatatggca 660
 ctactcgtcg ggactgactt caatgagggt gtaaaggggt atggcgcaag gaggggactc 720
 aaactcatca gggagaaggg cgacattttc aaagtcatca gggaccttga agctgacata 780
 ggtggcgacc cccaggtcct caggaggatc tttctggagc cagaggtttc agaggactat 840
 gagatcaggt ggagaaaacc tgacgtggaa ggtgttatcg agttcctgtg cactgaacac 900
 ggcttttcag aggaccgtgt gagggatgca cttaaaaaat ttgagggtgc atcctccacc 960
 cagaagagcc tggaggactg gttctga 987

<210> 183
 <211> 328
 <212> PRT
 <213> Methanobacterium thermoautotrophicum

<400> 183

Met	Gly	Val	Lys	Leu	Arg	Asp	Val	Val	Ser	Pro	Arg	Arg	Ile	Arg	Leu
1				5					10					15	
Glu	Asp	Leu	Arg	Gly	Arg	Thr	Val	Ala	Val	Asp	Ala	Ala	Asn	Thr	Leu
			20					25					30		
Tyr	Gln	Phe	Leu	Ser	Ser	Ile	Arg	Gln	Arg	Asp	Gly	Thr	Pro	Leu	Met
		35					40					45			
Asp	Ser	Arg	Gly	Arg	Val	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
	50					55					60				
Thr	Ala	Ala	Val	Met	Glu	Arg	Glu	Ile	Arg	Val	Ile	Tyr	Val	Phe	Asp
65					70					75					80
Gly	Arg	Ser	His	His	Leu	Lys	Gly	Glu	Thr	Val	Ser	Arg	Arg	Ala	Asp
				85					90					95	
Ile	Arg	Lys	Lys	Ser	Glu	Val	Glu	Trp	Lys	Arg	Ala	Leu	Glu	Glu	Gly
			100					105					110		
Asp	Ile	Asp	Arg	Ala	Arg	Lys	Tyr	Ala	Val	Arg	Ser	Ser	Arg	Met	Ser
		115					120					125			
Ser	Glu	Ile	Leu	Glu	Ser	Ser	Lys	Arg	Leu	Leu	Glu	Leu	Leu	Gly	Ile
	130					135					140				
Pro	Tyr	Val	Gln	Ala	Pro	Gly	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met
145					150					155					160
Val	Lys	Met	Gly	Asp	Ala	Trp	Ala	Val	Ala	Ser	Gln	Asp	Tyr	Asp	Cys
				165					170					175	
Leu	Leu	Phe	Gly	Ala	Pro	Arg	Val	Val	Arg	Lys	Val	Thr	Leu	Ser	Gly
			180					185					190		
Lys	Leu	Glu	Asp	Pro	His	Ile	Ile	Glu	Leu	Glu	Ser	Thr	Leu	Arg	Ala
		195					200					205			
Leu	Ser	Ile	Ser	His	Thr	Gln	Leu	Val	Asp	Met	Ala	Leu	Leu	Val	Gly
	210					215					220				
Thr	Asp	Phe	Asn	Glu	Gly	Val	Lys	Gly	Tyr	Gly	Ala	Arg	Arg	Gly	Leu
225					230					235					240
Lys	Leu	Ile	Arg	Glu	Lys	Gly	Asp	Ile	Phe	Lys	Val	Ile	Arg	Asp	Leu
				245					250					255	
Glu	Ala	Asp	Ile	Gly	Gly	Asp	Pro	Gln	Val	Leu	Arg	Arg	Ile	Phe	Leu
			260					265					270		
Glu	Pro	Glu	Val	Ser	Glu	Asp	Tyr	Glu	Ile	Arg	Trp	Arg	Lys	Pro	Asp
		275					280					285			
Val	Glu	Gly	Val	Ile	Glu	Phe	Leu	Cys	Thr	Glu	His	Gly	Phe	Ser	Glu
	290					295					300				

Asp Arg Val Arg Asp Ala Leu Lys Lys Phe Glu Gly Ala Ser Ser Thr
 305 310 315 320

Gln Lys Ser Leu Glu Asp Trp Phe
 325

<210> 184

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 184

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
 1 5 10 15

Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
 20 25 30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
 35 40 45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
 50 55 60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
 85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
 100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
 115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
 130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
 145 150 155 160

Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
 165 170 175

Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
 180 185 190

Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
 195 200 205

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220

Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335
 Trp Phe Lys Arg
 340

<210> 185
 <211> 326
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 185
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
 50 55 60
 Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
 85 90 95
 Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
 100 105 110
 Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
 115 120 125

Pro	Lys	Met	Val	Glu	Asn	Cys	Lys	Tyr	Leu	Leu	Ser	Leu	Met	Gly	Ile
130						135					140				
Pro	Tyr	Val	Glu	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met
145					150					155					160
Ala	Lys	Lys	Gly	Asp	Val	Trp	Ala	Val	Val	Ser	Gln	Asp	Tyr	Asp	Ala
				165					170					175	
Leu	Leu	Tyr	Gly	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Thr	Thr	Lys
			180						185				190		
Glu	Met	Pro	Glu	Leu	Ile	Glu	Leu	Asn	Glu	Val	Leu	Glu	Asp	Leu	Arg
		195					200					205			
Ile	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp
	210					215					220				
Tyr	Asn	Pro	Gly	Gly	Val	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu
225					230					235					240
Leu	Val	Arg	Ser	Gly	Val	Ala	Lys	Asp	Val	Leu	Lys	Lys	Glu	Val	Glu
				245					250					255	
Tyr	Tyr	Asp	Glu	Ile	Lys	Arg	Ile	Phe	Lys	Glu	Pro	Lys	Val	Thr	Asp
			260					265					270		
Asn	Tyr	Ser	Leu	Ser	Leu	Lys	Leu	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys
		275					280					285			
Phe	Leu	Val	Asp	Glu	Asn	Asp	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His
	290					295					300				
Val	Asp	Lys	Leu	Tyr	Asn	Leu	Ile	Ala	Asn	Lys	Thr	Lys	Gln	Lys	Thr
305					310					315					320
Leu	Asp	Ala	Trp	Phe	Lys										
				325											

<210> 186
 <211> 332
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 186															
Met	Gly	Val	Pro	Ile	Gly	Glu	Ile	Ile	Pro	Arg	Lys	Glu	Ile	Glu	Leu
1				5					10					15	
Glu	Asn	Leu	Tyr	Gly	Lys	Lys	Ile	Ala	Ile	Asp	Ala	Leu	Asn	Ala	Ile
			20					25					30		
Tyr	Gln	Phe	Leu	Ser	Thr	Ile	Arg	Gln	Lys	Asp	Gly	Thr	Pro	Leu	Met
		35					40					45			
Asp	Ser	Lys	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Leu	Phe	Tyr	Arg
	50					55					60				

Thr 65	Ile	Asn	Leu	Met	Glu 70	Ala	Gly	Ile	Lys	Pro 75	Val	Tyr	Val	Phe	Asp 80
Gly	Glu	Pro	Pro	Glu 85	Phe	Lys	Lys	Lys	Glu 90	Leu	Glu	Lys	Arg	Arg	Glu 95
Ala	Arg	Glu	Glu 100	Ala	Glu	Glu	Lys	Trp 105	Arg	Glu	Ala	Leu	Glu	Lys	Gly 110
Glu	Ile	Glu 115	Glu	Ala	Ala	Lys	Tyr 120	Ala	Lys	Arg	Val	Ser 125	Tyr	Leu	Thr
Pro	Lys 130	Met	Val	Glu	Asn	Cys 135	Lys	Tyr	Leu	Leu	Ser 140	Leu	Met	Gly	Ile
Pro 145	Tyr	Val	Glu	Ala	Pro 150	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met 160
Ala	Lys	Lys	Gly	Asp 165	Val	Trp	Ala	Val	Val	Ser	Gln	Asp	Tyr	Asp	Ala 175
Leu	Leu	Tyr	Gly 180	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Thr	Thr	Lys 190
Glu	Met	Pro 195	Glu	Leu	Ile	Glu	Leu 200	Asn	Glu	Val	Leu	Glu 205	Asp	Leu	Arg
Ile	Ser 210	Leu	Asp	Asp	Leu	Ile 215	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp
Tyr 225	Asn	Pro	Gly	Gly	Val 230	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu 240
Leu	Val	Arg	Ser	Gly 245	Val	Ala	Lys	Asp	Val 250	Leu	Lys	Lys	Glu	Val	Glu 255
Tyr	Tyr	Asp	Glu 260	Ile	Lys	Arg	Ile	Phe 265	Lys	Glu	Pro	Lys	Val	Thr	Asp
Asn	Tyr	Ser 275	Leu	Ser	Leu	Lys	Leu 280	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys
Phe	Leu	Val	Asp	Glu	Asn	Asp 295	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His 300
Val 305	Asp	Lys	Leu	Tyr	Asn 310	Leu	Ile	Ala	Asn	Lys 315	Thr	Lys	Gln	Lys	Thr 320
Leu	Asp	Ala	Trp	Phe 325	Lys	His	His	His	His	His	His	His	His	His	His

<210> 187

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 187

Met	Gly	Val	Gln	Phe	Gly	Asp	Phe	Ile	Pro	Lys	Asn	Ile	Ile	Ser	Phe
1				5					10					15	
Glu	Asp	Leu	Lys	Gly	Lys	Lys	Val	Ala	Ile	Asp	Gly	Met	Asn	Ala	Leu
			20					25					30		
Tyr	Gln	Phe	Leu	Thr	Ser	Ile	Arg	Leu	Arg	Asp	Gly	Ser	Pro	Leu	Arg
		35					40					45			
Asn	Arg	Lys	Gly	Glu	Ile	Thr	Ser	Ala	Tyr	Asn	Gly	Val	Phe	Tyr	Lys
	50					55					60				
Thr	Ile	His	Leu	Leu	Glu	Asn	Asp	Ile	Thr	Pro	Ile	Trp	Val	Phe	Asp
65					70					75					80
Gly	Glu	Pro	Pro	Lys	Leu	Lys	Glu	Lys	Thr	Arg	Lys	Val	Arg	Arg	Glu
				85					90					95	
Met	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Met	Lys	Glu	Ala	Ile	Lys	Lys	Glu
			100					105					110		
Asp	Phe	Glu	Glu	Ala	Ala	Lys	Tyr	Ala	Lys	Arg	Val	Ser	Tyr	Leu	Thr
		115					120					125			
Pro	Lys	Met	Val	Glu	Asn	Cys	Lys	Tyr	Leu	Leu	Ser	Leu	Met	Gly	Ile
	130					135					140				
Pro	Tyr	Val	Glu	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met
145					150					155					160
Ala	Ala	Lys	Gly	Ser	Val	Tyr	Ala	Ser	Ala	Ser	Gln	Asp	Tyr	Asp	Ser
				165					170					175	
Leu	Leu	Phe	Gly	Ala	Pro	Arg	Leu	Val	Arg	Asn	Leu	Thr	Ile	Thr	Gly
			180					185					190		
Lys	Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Glu	Ile	Lys	Pro	Glu
		195					200					205			
Leu	Ile	Ile	Leu	Glu	Glu	Val	Leu	Lys	Glu	Leu	Lys	Leu	Thr	Arg	Glu
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Lys	Leu	Ile	Glu	Leu	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Pro	Gly
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Gly	Ile	Lys	Gly	Ile	Gly	Leu	Lys	Lys	Ala	Leu	Glu	Ile	Val	Arg	His
				245					250					255	
Ser	Lys	Asp	Pro	Leu	Ala	Lys	Phe	Gln	Lys	Gln	Ser	Asp	Val	Asp	Leu
			260					265					270		
Tyr	Ala	Ile	Lys	Glu	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asn	Tyr
		275					280					285			
Asn	Leu	Val	Trp	Arg	Asp	Pro	Asp	Glu	Glu	Gly	Ile	Leu	Lys	Phe	Leu
	290					295					300				

Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
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Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
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Trp Phe Lys Arg
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<212> PRT

<213> Artificial Sequence

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Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
35 40 45

Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
50 55 60

Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
145 150 155 160

Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
165 170 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
180 185 190

Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
195 200 205

Ile	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp
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Tyr	Asn	Pro	Gly	Gly	Val	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu
225					230					235					240
Leu	Val	Arg	Ser	Gly	Val	Ala	Lys	Asp	Val	Leu	Lys	Lys	Glu	Val	Glu
				245					250					255	
Tyr	Tyr	Asp	Glu	Ile	Lys	Arg	Ile	Phe	Lys	Glu	Pro	Lys	Val	Thr	Asp
			260					265					270		
Asn	Tyr	Ser	Leu	Ser	Leu	Lys	Leu	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys
		275					280					285			
Phe	Leu	Val	Asp	Glu	Asn	Asp	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His
	290					295					300				
Val	Asp	Lys	Leu	Tyr	Asn	Leu	Ile	Ala	Asn	Lys	Thr	Lys	Gln	Lys	Thr
305					310					315					320
Leu	Asp	Ala	Trp	Phe	Lys										
				325											